

Wed Oct 23 08:22:47 2002

GenStore version 5.1.3  
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OM nucleotide - nucleic search, using sw model  
Run on: October 22, 2002, 08:46:06 ; Search time 3976 Seconds  
(without alignments)  
17294.919 Million cell updates/sec  
Title: US-09-904-389-1  
Perfect score: 4286  
Sequence: 1 attcattatcagagagagga.....aaaaaaaaaaaaaaaaaaaaa 3286  
Scoring table: IDENTITY\_NDC  
Gapop 10.0 ; Gapext 1.0  
Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database :  
1: gb\_bar:\*  
2: gb\_htd:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_bar:\*  
16: em\_hum:\*  
17: em\_hum:\*  
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19: em\_mu:\*  
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21: em\_or:\*  
22: em\_yl:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htd\_hum:\*  
31: em\_htd\_inv:\*  
32: em\_htd\_of\_her:\*  
33: em\_htd\_inv:

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
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1	1195.6	36.4	3121	8	AY032953	AY032953, Rosa hybrid cultivar, 3121 bp, abba, cinn, 11N, 22 MAY 2002
2	996.8	30.3	2829	8	AF096250	AF096250, Rosa hybrid cultivar, 2829 bp, abba, cinn, 11N, 22 MAY 2002
3	996.8	30.3	2917	8	LE1Y8K1NA	LE1Y8K1NA, Rosa hybrid cultivar, 2917 bp, abba, cinn, 11N, 22 MAY 2002
4	979.2	29.8	2846	8	AF110518	AF110518, Rosa hybrid cultivar, 2846 bp, abba, cinn, 11N, 22 MAY 2002
5	898.8	27.4	3043	6	114046	114046, Rosa hybrid cultivar, 3043 bp, abba, cinn, 11N, 22 MAY 2002
6	898.8	27.4	3033	6	114046	114046, Rosa hybrid cultivar, 3033 bp, abba, cinn, 11N, 22 MAY 2002
7	898.8	27.4	3033	6	114046	114046, Rosa hybrid cultivar, 3033 bp, abba, cinn, 11N, 22 MAY 2002
8	856.6	26.1	2767	8	AF110519	AF110519, Rosa hybrid cultivar, 2767 bp, abba, cinn, 11N, 22 MAY 2002
9	439.4	13.4	1795	8	AF386508	AF386508, Rosa hybrid cultivar, 1795 bp, abba, cinn, 11N, 22 MAY 2002
10	342.8	10.4	3158	8	AF305911	AF305911, Rosa hybrid cultivar, 3158 bp, abba, cinn, 11N, 22 MAY 2002
11	342.8	10.4	3388	8	AF305912	AF305912, Rosa hybrid cultivar, 3388 bp, abba, cinn, 11N, 22 MAY 2002
12	339.4	10.3	3456	8	AF305913	AF305913, Rosa hybrid cultivar, 3456 bp, abba, cinn, 11N, 22 MAY 2002
13	323.2	9.8	3081	8	AF247567	AF247567, Rosa hybrid cultivar, 3081 bp, abba, cinn, 11N, 22 MAY 2002
14	311.4	9.5	633	8	AF141419	AF141419, Rosa hybrid cultivar, 633 bp, abba, cinn, 11N, 22 MAY 2002
15	308.2	9.4	1521	8	AY029067	AY029067, Rosa hybrid cultivar, 1521 bp, abba, cinn, 11N, 22 MAY 2002
16	283.2	8.6	681	8	AY062764	AY062764, Rosa hybrid cultivar, 681 bp, abba, cinn, 11N, 22 MAY 2002
17	270.2	8.2	2392	8	AY056257	AY056257, Rosa hybrid cultivar, 2392 bp, abba, cinn, 11N, 22 MAY 2002
18	270.2	8.2	2824	8	AY074498	AY074498, Rosa hybrid cultivar, 2824 bp, abba, cinn, 11N, 22 MAY 2002
19	267.8	8.1	2923	8	AY074498	AY074498, Rosa hybrid cultivar, 2923 bp, abba, cinn, 11N, 22 MAY 2002
20	260.8	7.9	564	8	AF261147	AF261147, Rosa hybrid cultivar, 564 bp, abba, cinn, 11N, 22 MAY 2002
21	242.8	7.4	2837	8	AY059769	AY059769, Rosa hybrid cultivar, 2837 bp, abba, cinn, 11N, 22 MAY 2002
22	208	6.3	339	8	AF387794	AF387794, Rosa hybrid cultivar, 339 bp, abba, cinn, 11N, 22 MAY 2002
23	158.4	4.8	348	8	AF261148	AF261148, Rosa hybrid cultivar, 348 bp, abba, cinn, 11N, 22 MAY 2002
24	156.2	4.8	3181	8	AY049428	AY049428, Rosa hybrid cultivar, 3181 bp, abba, cinn, 11N, 22 MAY 2002
25	155.2	4.7	6295	6	114048	114048, Rosa hybrid cultivar, 6295 bp, abba, cinn, 11N, 22 MAY 2002
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27	155.2	4.7	6312	6	114047	114047, Rosa hybrid cultivar, 6312 bp, abba, cinn, 11N, 22 MAY 2002
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35	155.2	4.7	6312	8	AT1671R18	AT1671R18, Rosa hybrid cultivar, 6312 bp, abba, cinn, 11N, 22 MAY 2002
36	155.2	4.7	102897	8	AT1671R18	AT1671R18, Rosa hybrid cultivar, 102897 bp, abba, cinn, 11N, 22 MAY 2002
37	125.8	4.8	2122	8	AY070086	AY070086, Rosa hybrid cultivar, 2122 bp, abba, cinn, 11N, 22 MAY 2002
38	122	4.7	1610	8	FSY298992	FSY298992, Rosa hybrid cultivar, 1610 bp, abba, cinn, 11N, 22 MAY 2002
39	118.2	4.6	1584	3	DD1297466	DD1297466, Rosa hybrid cultivar, 1584 bp, abba, cinn, 11N, 22 MAY 2002
40	106	3.2	1724	8	SOYPRORIN	SOYPRORIN, Rosa hybrid cultivar, 1724 bp, abba, cinn, 11N, 22 MAY 2002
41	106	3.2	2280	8	AY062096	AY062096, Rosa hybrid cultivar, 2280 bp, abba, cinn, 11N, 22 MAY 2002
42	103.4	3.1	2271	8	AF462860	AF462860, Rosa hybrid cultivar, 2271 bp, abba, cinn, 11N, 22 MAY 2002
43	101.4	3.1	561	8	AF271206	AF271206, Rosa hybrid cultivar, 561 bp, abba, cinn, 11N, 22 MAY 2002
44	100.4	3.1	1168	8	AY063013	AY063013, Rosa hybrid cultivar, 1168 bp, abba, cinn, 11N, 22 MAY 2002
45	100.4	3.1	2108	8	AY035004	AY035004, Rosa hybrid cultivar, 2108 bp, abba, cinn, 11N, 22 MAY 2002

ALIGNMENTS			
RESULT 1	AY032953	3121 bp	abba, cinn, 11N, 22 MAY 2002
LOCUS	Rosa hybrid cultivar	3121 bp	abba, cinn, 11N, 22 MAY 2002
DEFINITION	Rosa hybrid cultivar	3121 bp	abba, cinn, 11N, 22 MAY 2002
ACCESSION	AY032953	3121 bp	abba, cinn, 11N, 22 MAY 2002
VERSION	AY032953.1	3121 bp	abba, cinn, 11N, 22 MAY 2002
KEYWORDS	GI:13946470	3121 bp	abba, cinn, 11N, 22 MAY 2002
SOURCE	Rosa hybrid cultivar	3121 bp	abba, cinn, 11N, 22 MAY 2002
ORGANISM	Rosa hybrid cultivar	3121 bp	abba, cinn, 11N, 22 MAY 2002
REFERENCE	1 (bases 1 to 3121)	3121 bp	abba, cinn, 11N, 22 MAY 2002
AUTHORS	Owen, C.A., Mueller, R.K. and Stumm, R.M.	3121 bp	abba, cinn, 11N, 22 MAY 2002
TITLE	Direct Submission	3121 bp	abba, cinn, 11N, 22 MAY 2002
JOURNAL	Submitted (23-APR-2001) Horticultural Genetics and Molecular Biology	3121 bp	abba, cinn, 11N, 22 MAY 2002
FEATURES	Location/Qualifiers	3121 bp	abba, cinn, 11N, 22 MAY 2002
source	1..3121	3121 bp	abba, cinn, 11N, 22 MAY 2002
organism	"Rosa hybrid cultivar"	3121 bp	abba, cinn, 11N, 22 MAY 2002
taxon	"taxon:128745"	3121 bp	abba, cinn, 11N, 22 MAY 2002



























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 DB 1416 AGATAAAGAAATGTCACATTTCTAAATATGTAATATGTCGAAGTATGTTAAACGACAGTGA 1472  
 QY 1608 TTTTCTAGAAAAATGTTAGTGGCTTTAAGGCAATATCTACACACATTTGGTCTGGAAGATTCGGA 1727  
 DB 1474 CATGACAGAGAAACAGGTTCTTCTGAACATGTTCTCCATTCGGGGAAGATGC----- 1526  
 QY 1728 GATCTCTTAGATTTCTGTCATGTAAGGATGATCATGTTAAGAAATTTAGCATTTGTCTCA 1787  
 DB 1527 ---TCAATCAGAGATACAGACGACGATATACATTAATGATGATACGCTTCTTCTGCTGAGT 1583  
 QY 1788 TGATGATGATTTGATATAGAAAAACAA---ATGAGCTTTCCTTGGCTTACAGAAATTTGGT 1844  
 DB 1584 AGGATGATGTTTCTGCTATACAGATGAAAGATCTATGTCATGATGATGATGATGATGATGATGAT 1643  
 QY 1845 TATGAT 1904  
 DB 1644 TATGAT 1703  
 QY 1905 ATATGAT 1964  
 DB 1704 TATGAT 1763  
 QY 1965 GAT 2024  
 DB 1764 TATGAT 1823  
 QY 2025 TATGAT 2084  
 DB 1824 TATGAT 1883  
 QY 2085 GAT 2141  
 DB 1884 GAT 1943  
 QY 2142 TATGAT 2201  
 DB 1944 TATGAT 2003  
 QY 2202 TATGAT 2261  
 DB 2004 TATGAT 2063  
 QY 2262 TATGAT 2321  
 DB 2064 TATGAT 2323  
 QY 2322 TATGAT 2381  
 DB 2124 TATGAT 2183  
 QY 2482 TATGAT 2441  
 DB 2184 TATGAT 2243  
 QY 2442 TATGAT 2501  
 DB 2244 TATGAT 2303  
 QY 2502 TATGAT 2561  
 DB 2304 TATGAT 2363  
 QY 2362 TATGAT 2421  
 DB 2464 TATGAT 2423  
 QY 2422 TATGAT 2481  
 DB 2424 TATGAT 2483

QY 2682 GTGACAAATCTGTG 2694  
 DB 2484 ATGAATCTGTG 2496  
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 LOCUS  
 DEFINITION  
 Pirus communis putative serine/threonine-specific protein kinase  
 (CTR1) mRNA, partial cds.  
 ACCESSION  
 AF386508  
 VERSION  
 AF386508.1  
 GI:18252316  
 SOURCE  
 Pirus communis  
 ORGANISM  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;  
 Rosidae; eucosids I; Rosales; Rosaceae; Maloideae; Pyrus;  
 1 (bases 1 to 1795)  
 El Sharkawy, I., Li, Z.G., Latche, A. and Lelievre, J.M.  
 Ripening related genes in pear (*Pyrus communis*)  
 Unpublished  
 REFERENCE  
 2 (bases 1 to 1795)  
 El Sharkawy, I., Li, Z.G., Latche, A. and Lelievre, J.M.  
 Direct Submission  
 Submitted (30-MAY-2001) Biologie Moléculaire et Physiologie de la  
 Maturation des Fruits, INP - ENSA, Av. de l'Agriculture 63122  
 Castanet Tolosan Cedex 43426, France  
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 /submitter "Basse-Cassagne"  
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 VDFHQQLEDFLEVAKKKVL DHHVLEKGVAKRPHLSITVLEKSLVRLHR  
 PASPTI DPEPPI ELAI VAAQD NY DFLNLEVHRL EELNLSKVAAY DPH  
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 BASE COUNT 482 a 359 c 436 g 518 t  
 ORIGIN  
 Query Match 13.48% Score 439.41 DB 81 Length 1795  
 Best Local Similarity 68.98% Prod. No. 5.4e-97  
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 DB 692 TCACCGAATCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 761  
 QY 1875 GAAATATGAGATAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1934  
 DB 752 GAT 811  
 QY 1935 TATGAT 1994  
 DB 812 TGTGTTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871  
 QY 1995 AGAGTGGAT 2054

[illegible]









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QY 2374 CTACGGATCAACATCAAAATGAAAGTACATGCTTTACAGCTTTGGAGTGATTTTGTGG 2433
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QY 914 TTGAGAAATCAACCGGTAAATGACAAATGACGCTGTACAGCTTTGGTGCATATTTGG 973
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2434 GAGTGGTAACTTTGGTAACAGCAAGGTGTAATCTAAACCCAGCTCAGCTTGTGGAGCT 2493
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 974 GAATTAAGTACTTCAAGCTTCGCTGSAAGGTTTGAACCGGATGCAAGTGTGGAGCT 1033
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2494 GTTGGATTTAAGGCCAAAGGCTTGACATGCCAGCTGATGTAATGCCAAATGGCTTCC 2553
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1034 GTCGATTCAGAAATGACAGGCTTGAAATGCCAGATGATCGATCTAACTGTGGCAG 1093
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2554 TTAATAGTGGCTTGTGTGAGGATGAGGCAATGSAAGGCTGCTTTTCCAGCAATAG 2613
DB      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1094 ATAATCGGTGAATGTGTGGCAAGGCAACCAATTAGCGGCATCGTTTACACAGCTGATG 1153
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QY 2614 GAAAGCTTGAAG 2626
DB      | | | | | | | |
QY 1154 CAAAGTTTGAAG 1166
DB      | | | | | | | |
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Search completed: October 22, 2002, 09:53:16  
Job time : 4007 secs

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QY 2038 ATGAAATGTTTAAAGACATGTAATATTTGACATGTTTATGAGTGGGGAGAAAGACCA 2067  
 DB 1915 AAGAAAGGCTTCGGACAGCAAGCAATGTTCTTTCATGCGTGGGAGATCAACCTCCA 1974  
 QY 2068 AACTGTCATGTTGACAGCAATATCTATGACAGAGTGTATGATAGCTTTTGCATAAG 2127  
 DB 1975 AATTGTCATGTTGACAGCAATATCTATGACAGAGTGTATGATAGCTTTTGCATAAA 2034  
 QY 2129 TACAGTCCA AAGACATAGTGAACACCTCCCAATAAATATGCTTTTATATGCTGA 2184  
 DB 2045 AGTGGAGCAAGAGCAATTAATGACAGACCTGGCTGAGTATGCTTATGATGCTT 2094  
 QY 2185 AAGCAATGAACTACTGACAGAGAGTGTATGCTCAATGCTGATGCTGATTTAAATGA 2244  
 DB 2095 AAGCAATGAACTACTGACAGAGAGTGTATGCTCAATGCTGATGCTGATTTAAATGA 2154  
 QY 2245 GGAATCTGTTAGTTCAGCAAGAGTATACAGTCAAGTGTGCTGATTTGCTGCTGCT 2304  
 DB 2155 CAAACTTATGTTGACAGCAAGAGTGTATGCTCAAGTGTGCTGCTGCTGCTGCT 2214  
 QY 2305 TTAAGGACAGCAATTTCTTTCATCCAAATGTCAGAGTGGACACCTCAATGCTGCTG 2364  
 DB 2215 TTAAGGACAGCAATTTCTTTCATCCAAATGTCAGAGTGGACACCTCAATGCTGCTG 2274  
 QY 2365 CAGAACTACTAGGAGTATGAGTCAATGAAAGTCAATGCTGCTGCTGCTGCTGCT 2424  
 DB 2275 CAGAACTACTAGGAGTATGAGTCAATGAAAGTCAATGCTGCTGCTGCTGCTGCT 2334  
 QY 2425 ATTGTTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2484  
 DB 2335 ATTGTTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2394  
 QY 2485 GTCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2544  
 DB 2395 GTCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2454  
 QY 2545 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2604  
 DB 2455 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2514  
 QY 2605 AATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2664  
 DB 2515 AATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2574  
 QY 2665 GA 2666  
 DB 2575 GA 2576

RESULT 2  
 AAQ98816  
 ID AAQ98816 standard; cDNA: 3033 BP.

AC AAQ98816;

XX 19-JAN-1996 (first entry)

XX Arabidopsis CTR1 cDNA.

DE CTR1: constitutive triple response; transgenic plant; ethylene;  
 KW stress tolerance; crop improvement; ss.

OS Arabidopsis thaliana ecotype Columbia.

XX Key Location/Qualifiers  
 PH 118..2583  
 FT /\*lag= a

DN US5444166-A.

XX 22-AUG-1995.

XX

PF 10-AUG-1992; 9205-0928464.  
 XX  
 PR 12-JAN-1993; 9305-0003311.  
 DR 10-AUG-1992; 9205-0928464.  
 XX  
 PA (OYPE-) UNIV PENNSYLVANIA.  
 XX  
 XX Ecker JR, Kieber JJ;  
 XX WPI; 1995-30215239.  
 DB P-PSDB; AAR80574.  
 XX  
 PT New constitutive triple response genes and mutants - isolated from  
 FT Arabidopsis thaliana, used to produce transgenic plants with  
 PT improved properties  
 XX  
 PS Claim 1; Column 21-28; 41pp; English.  
 XX  
 CC The CTR1 gene was mapped to an interval between 2 RFLPs in  
 CC chromosome 5 of A. thaliana and a chromosome walk in this area was  
 CC initiated using a YAC library. 2 clones were isolated and used to  
 CC probe a cDNA library derived from polyA RNA from 3-day-old dark-  
 CC grown, ethylene treated A. thaliana seedlings. The cDNA for the  
 CC CTR1 gene is given in AAC38816. Expression of the CTR1 gene in  
 CC transgenic plants results in a dominant ethylene insensitive  
 CC phenotype.  
 XX  
 SQ Sequence 3033 BP; 797 A; 605 C; 751 G; 880 T; 0 other;

Query Match 27.4%; Score 898.8; DB 16; Length 3033;  
 Best Local Similarity 64.3%; Pred. No. 6,96-242;  
 Matches 158; Conservative 0; Mismatches 684; Indels 216; Gaps 7;

QY 253 AAGAGGAGAGATGATAGAGTGTGTTTATGCTGATGCTGATGCTGATGCTGATGCTG 412  
 DB 283 AAGAGGAGATGATAGAGTGTGTTTATGCTGATGCTGATGCTGATGCTGATGCTG 412  
 QY 313 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 466  
 DB 343 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 466  
 QY 467 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 426  
 DB 403 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 426  
 QY 427 AACGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 469  
 DB 462 AACGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 469  
 QY 487 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 518  
 DB 520 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 518  
 QY 514 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567  
 DB 580 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567  
 QY 568 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627  
 DB 640 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640  
 QY 628 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
 DB 700 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 700  
 QY 688 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 747  
 DB 760 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 747  
 QY 748 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
 DB 820 ATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807













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XX OS Arabidopsis thaliana.
XX FH
XX Key Location/Qualifiers
XX mutation 2347..2348
XX /*tag= a
XX /*note= "Site of X-ray-generated deletion of
XX nucleotides 2348-2364 (GTCTCTTAATCTGTTT)
XX from wild-type ctr genomic sequence AAQ57912"
XX W09404047-A.
XX XX
XX 17-FEB-1994.
XX XX
XX 05-AUG-1993; 93WO-US07347.
XX XX
XX 10-AUG-1992; 92US-0928464.
XX XX
XX (DYPE-) UNIV PENNSYLVANIA.
XX FH
XX Ecker JR, Kieber JJ;
XX BP1; 1994 065280/08.
XX XX
XX Constitutive triple response genes and ctr mutants - exhibit
XX phenotype resulting from exposure to ethylene in wild type
XX plants, eq in response to stress
XX XX
XX Claim 4; Page 48-53; 69pp; English.
XX XX
XX A cDNA clone (AAQ57911) and a genomic clone (AAQ57912) coding for the
XX wild-type constitutive triple response (CTR) gene in plants have
XX been isolated. The ctr gene encodes a protein resembling the Raf
XX family of serine/threonine kinases. The ctrl-2 mutation (AAQ57913)
XX has a 17bp deletion from nucleotide 2348 to 2364 of the CTR genomic
XX DNA sequence. The mutation was generated by X-ray mutagenesis and
XX results in a constitutive "ethylene" phenotype.
XX XX
XX Sequence 5973 BP; 1664 A, 1052 C; 1238 G; 1919 T; 0 other;
XX XX
XX Query Match 4.7%; Score 155.2; DB 15; Length 5873;
XX Best local similarity 69.4%; Pred. No. 4e-31;
XX Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGATGATGATCAATATTGGAGAAAGTGGGATGTTTATCTAATTCATGG 752
DB 1176 GGTAAATGATGATGATCAATATTGGAGAAAGTGGGATGTTTATCTAATTCATGG 752
QY 753 GATGAGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 812
DB 1246 TCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 812
QY 813 ATTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 872
DB 1296 AATTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1355
QY 873 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 932
DB 1456 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1415
QY 933 CATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
DB 1416 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1475
QY 993 GAGG 996
DB 1476 GAGG 1479
XX XX
XX RESULT 8
XX AAQ57912
XX 10 AAQ57912 standard; DNA; 5890 BP.
XX XX

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AAQ57912:
AC XX
XX 08-SEP-1994 (first entry)
XX DE Arabidopsis thaliana constitutive triple response gene.
XX KW Constitutive triple response gene; ctr; ethylene phenotype;
XX KW plant hormone; stress response; constitutive mutant;
XX KW serine kinase; threonine kinase; raf family; transgenic plant; ss.
XX OS Arabidopsis thaliana.
XX FH
XX Key Location/Qualifiers
XX intron 1..353
XX exon /*tag= a
XX 354..1001
XX /*tag= b
XX intron /number= 1
XX 1002..1176
XX /*tag= c
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XX 1478..1574
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XX 1575..1719
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XX /*tag= g
XX 1937..2038
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XX 2174..2379
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XX 2380..2736
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XX 3520..3588
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XX /number= 8
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XX /number= 11
XX 4137..4369
XX /*tag= w
XX 4370..4438
XX /*tag= x
XX /number= 12

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cv Seeds of A. thaliana ecotype Columbia were subjected to  
 cv diploxytane mutagenesis and screened for mutants that  
 cv constitutively displayed the triple response by plating on agar in the  
 cv absence of added ethylene in the dark. Sequence analysis of isolated  
 cv mutant eth1-1 genomic DNA (given in AAQ98820) indicated a T to A point  
 cv mutation at a position corresp. to position 4800 of the wild-type  
 cv genomic sequence (AAQ9817). Transgenic plants expressing recessive  
 cv eth1 mutations resemble ethylene treated wild-type plants.  
 XX  
 SQ Sequence 6312 bp; 1818 A; 1107 C; 1296 G; 2091 T; 0 other;

Query Match	4.7%	Score 155.2;	DB 16;	Length 6312;
Best Local Similarity	69.4%	Prod. No. 4.2e-31;		
Matches 211;	Conservative 0;	Mismatches 93;	Indels 0;	Gaps 0;

  

QY	693	GGTAAATGATGCAATGTCATATTTGAGAGAAAGTGGTGAATGGTTTTTAATCTAATTCATGG	752
DB	1598	GGTTAAATGCTGCTTATGCTATTAATGATAAAGTCTGATGGGTTTTTATATGATGAAATGG	1657
QY	753	GATGCAATCAATATGATGCTGATTAATGCAATGCTGGCAAGAGAGAGAGGGGTATACCAAC	812
DB	1658	TCTGATGCTGCTATTTGGAGCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATG	1717
QY	813	ATTGCAATCTGTGAAACACAGTTCATTCAGATGCTTCATGCAATTCGAATAGTCTTTCAT	872
DB	1718	AATTCAAATCAATACAGAGCTGTGATTTCTGGCTTCATCTTCCTTGAAGCGATCATAGT	1777
QY	873	AGATGGGATATATGATGATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	932
DB	1778	GGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1837
QY	933	CAGTGTGCTAAGCAATAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	992
DB	1838	TAGTGTGATTAACACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1897
QY	993	GGGG 996	
DB	1898	GGGG 1901	

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 Job time : 4.03 secs









South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-530-4363 or contact via email: ccu@resgen.com  
Insert length: 1098 Std Error: 0.00  
High quality sequence stop: 41  
Location/Qualifiers  
1..581

# FEATURES

SOURCE

1..581

Genbank "Cloning 582"  
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/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-2205"  
/tissue\_type="Hypocotyl", 9 10 day old etiolated seedlings"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK(-) Site 1; EcoRI, Site 2;  
XhoI: This cDNA library was constructed from mRNA isolated  
from etiolated hypocotyl tissue of 9 10 day old seedlings  
of the cultivar Williams 82. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) primer with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt ended cDNA fragments  
followed by digestion with EcoRI and XhoI. The cDNA  
fragments were directionally cloned into the EcoRI-XhoI  
restriction site of the pBluescript vector. The ligated  
cDNA fragments were transformed into DH10B host cells  
(Gibco BRL). This library was constructed by Dr. Randy  
Shormaker."

BASE COUNT 150 a 109 c 146 q 176 t

ORIGIN

Query Match 11.18; Score 461.4; DB 10; Length 581;  
Best Local Similarity 77.8%; Pred. No 276 59;  
Matches 452; Conservative 0; Mismatches 137; Indels 3; Gaps 1.  
QY 1925 GCTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1984  
DB 1 GCTGAGATGCTGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1985 AGTTCTGACAGACAGTGTGTATCATCAAAATCTTACGACATCTCTAAATGATGATGTTA 2044  
DB 1 AGTTCTGACAGACAGTGTGTATCATCAAAATCTTACGACATCTCTAAATGATGATGTTA 120  
QY 2045 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2104  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 180  
QY 2105 GCTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2164  
DB 1 GCTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2165 TAAATATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2224  
DB 1 TAAATATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2225 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2284  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2285 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2344  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2345 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2404  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2405 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2464  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2465 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2524  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240  
QY 2525 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 2584  
DB 1 TGGTGTGATGCTGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 240

# RESULTS

BP919922

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

1..596

Genbank "Cloning 596"

/db\_xref="gi:1004599"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-2205"

/tissue\_type="Hypocotyl", 9 10 day old etiolated seedlings"

/lab\_host="DH10B"

/note="Vector: pBluescript II SK(-) Site 1; EcoRI, Site 2;  
XhoI: This cDNA library was constructed from mRNA isolated  
from etiolated hypocotyl tissue of 9 10 day old seedlings  
of the cultivar Williams 82. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) primer with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt ended cDNA fragments  
followed by digestion with EcoRI and XhoI. The cDNA  
fragments were directionally cloned into the EcoRI-XhoI  
restriction site of the pBluescript vector. The ligated  
cDNA fragments were transformed into DH10B host cells  
(Gibco BRL). This library was constructed by Dr. Randy  
Shormaker."

BASE COUNT 150 a 109 c 146 q 176 t

ORIGIN

Query Match 10.98; Score 456.4; DB 10; Length 596;  
Best Local Similarity 75.8%; Pred. No 234 59;  
Matches 447; Conservative 0; Mismatches 147; Indels 0; Gaps 0.  
QY 951 CATCAATGAAATGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 910  
DB 2 CATCAATGAAATGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 911 ACAGGCTGATATATATTTCTGTAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 970  
DB 2 ACAGGCTGATATATATTTCTGTAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 971 CAAAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1030  
DB 2 CAAAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1031 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1090  
DB 2 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1091 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1150  
DB 2 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1151 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1210  
DB 2 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1211 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1270  
DB 2 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60  
QY 1271 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 1330  
DB 2 CAGAGCTGATGCTGAAGATCTCTACAGAAAGACACTTCTATCTGTAAGCTGTAAAG 60





[illegible][illegible]

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Local ion/Qualifiers
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/cclone "GENOME SYSTEMS clone ID: Sacc04-44.2"
/clone_id "Gm c1941"
/tissue_type "Williams seedlings, during the vegetative phase"
/lab_host "PH10R"
/vector "pUC19 phagemid plasmid; E. coli strain JM103"
From whole Williams Seedlings, which were infected with Agrobacterium tumefaciens strain AGL1, which was prepared on paper towels with distilled water for 5 days, incubated at 40 degrees C for 1 hour. The cotyledons were removed and the remaining tissue was flash frozen in liquid nitrogen. StrataGene's cDNA Synthesis Kit (catalog number 2004-3) was used. cNA Synthetize the cDNA. First strand synthesis was performed with 5-methyl dH2O, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V A G or G) was added to the 3' end of the primer [GAACAGACAAGACAAAGAATTAATCAT(1)P] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with cloned phi DNA, ligated to EcoRI adapters and subsequently classified. The cDNA was then

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1 CURRENT APPLICATION DATA:  
 2 APPLICATION NUMBER: 03/29/003, 4118  
 3 FILING DATE: January 12, 1994  
 4 CLASSIFICATION: 800  
 5 PRIOR APPLICATION DATA:  
 6 APPLICATION NUMBER: 07/928,464  
 7 FILING DATE: August 10, 1992  
 8 ATTORNEY/AGENT INFORMATION:  
 9 NAME: LOUI Y. Beardsell  
 10 REGISTRATION NUMBER: 34,293  
 11 REFERENCE/KEY NUMBER: RIN 1108  
 12 TELECOMMUNICATION INFORMATION:  
 13 TELEPHONE: 215-568-4109  
 14 TELEFAX: 215-568-4439  
 15 INFORMATION FOR SEQ ID NO: 4:  
 16 SEQUENCE CHARACTERISTICS:  
 17 LENGTH: 6312 base pairs  
 18 TYPE: nucleic acid  
 19 STRANDEDNESS: single  
 20 ORIENTATION: linear  
 21 MOLECULE TYPE: DNA (genomic)  
 22 US-08 003 4118-4

Query Match 4.78; Score 155.2; DB 1; Length 6312;  
 Best Local Similarity 69.48; Prod. No. 2.6e+32;  
 Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;  
 QY 693 GATAAATGACGATGCTATATTTGATGAAAGTGGTGAATGGTTTATCTAAATTCATGG 752  
 DB 1598 GTTAAATGGTGTCTAATGAGTATGATAAAGTTCTGATGGTTTATATGATGAATGG 1657  
 QY 783 GATGAGATCATATGATGTGATTAAGTACCAATCTGTAAGAGGATGGGGATATATATC 812  
 DB 1658 TCTGATATCTATATTTGACCTTAAGGATATCGAATGATGAAAGTGGTGGATCCCTTC 1717  
 QY 813 ATTGAAATCTTGAAATAGTTGATGTTTAAATATCGTGTATCAATGAAATAGTTTIGAT 872  
 DB 1718 AATGAAATCATTAAGTATGTTGATGTTTCTGTTGATTTGATTTGCTTGGAAATCATAC 1777  
 QY 874 AGATGGGTATATGATGCTAGCTTAATAAAGCAATCTGCAAAAGAGGGTGTATATAATTTCTTC 942  
 DB 1778 GATAAGGCTGATGATGATCTTCAAGCAAACTTAAAGAGAGTGTAACTATATCTTG 1837  
 QY 943 CAGTTGGTTAAGCAAAAGAGGTTCTGATGATATATAGCAAAAGCTGGTATGCAATGACTT 992  
 DB 1838 TAGCTGTATTAACCAAAAGAGGTTGTTGATGAGCTGGCAAAAGCTTATCTGCAATGCTAT 1897  
 QY 993 AAAAG 996  
 DB 1898 AAAAG 1901

Search completed: October 22, 2002, 10:42:30  
 Job time: 3.125 secs







DT	13-MAR-2001 (first entry)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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13-MAR-2001 (first entry)  
 Arabidopsis thaliana CTRL.  
 Arabidopsis thaliana; EPR1; enhanced disease resistance; anti-fungal; antibacterial; gene therapy; transgenic plant; pathogen; EPR1; ss.  
 Arabidopsis thaliana.  
 W0200071696-A1.  
 30-NOV-2000.  
 26-MAY-2000: 200000-US14718.  
 26-MAY-1999: 990S-0135895.  
 (ADRE ) ADVANCED RES & TECHNOLOGY INST.

Innes RW, Frye CA;

WPI: 2001-025156/03

New gene EPR1 of Arabidopsis thaliana, the disruption of which enhances disease resistance in plants, is useful for producing transgenic plants and mutants having increased resistance to plant pathogens

Example 2: Page 76-78; 91pp; English.

The present sequence is given in a specification relating to the EPR1 gene located on Arabidopsis thaliana chromosome 1 between markers A16A11 and M231. The disruption of the EPR1 gene is associated with enhanced resistance of a plant to plant pathogens or other disease-causing agents. A mutated transgene comprising the EPR1 gene mutated at residue 696 of the 821 amino acid coding domain may be introduced into the plant genome to reduce expression of EPR1. Alternatively, a transgene that expresses part or all of an antisense strand of the EPR1 gene may be introduced. A transgene which expresses a sense strand of the EPR1 gene may be introduced to produce fertile Arabidopsis thaliana plants. Transgenic plants exhibiting the desirable phenotypes of lack of EPR1 protein, EPR1 mRNA, or enhanced resistance to plant pathogens can be used for plant breeding, or directly in agricultural or horticultural applications. Plants containing one transgene may also be crossed with plants containing a complementary transgene in order to produce plants with enhanced or combined phenotypes. EPR1 nucleic acids may be used as probes to detect the presence and/or expression of EPR1 genes and to identify related genes from other plant species.

Seq Sequence 821 AA;

Query Match 61.99; Score 2742.5; DB 22; Length 821;  
 Best local similarity 62.39; Prod. No. 3.5e 245;  
 Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;

QY 1 MEMEPSPSYSLISQIPPEFW3-----TGASTSFYNSVAA-----GNNVTKPTDR-VFD 49  
 DB 1 MEMEGRSNTLLSQSLEQVSVSVTCAPPPIIDYSSSESPSNHNSGNTGRKAKAERGEGD 60  
 QY 50 WD-----GSDHPLNTQAYRIG-NLY-SWGLGRHSKSSSYDDSSISDYAYAPTISNPAAN 103  
 DB 61 WDPSGSGGGBBBLNRQTEYGRMYASTNLRSSSSSTFSSSSLSGYYMELT-AAAR 119  
 QY 104 EIMALEYLLDPTFV-----MFAVSNZ-SSQF-SWAGQFSPFSPQDQPI-VL 150  
 DB 120 EIESVGFQPDGPRGFGAGGADLRIGMAADSAAGSSSKSWAQQTRESYQLQALALRF 179  
 QY 151 SSXTCALDPNMDPDPDEAALRSLISAEALSHRWNGMGMSYLEKVPDQGYLLHGMDP 210  
 DB 180 SSEATKADDPNFDVPPDESALRTSPSSAETVSHRPFWNGGCLSYDYDKVHDGFMNGDLP 239  
 QY 211 YVNSLQNLGPDGKPSFESKIVSSIGSSIGSSLEVVLDHESLASLKLONKRVNLSSSCV 270  
 DB 240 YTWLCLDLHESGEPSPLESFAPVSDSSI FALIVPPSPAPKELNPNVPISSQCI 299  
 QY 271 TTREVALHIAKLVNMLDGSSEGEDELVEAWKKESTDEGFPDGSAAVPIPGISVGLPH 330  
 DB 300 TTREVNQLAKLNNRMGPVIMGEDELVPWKKKEIDGLKE-IFKVVVPDGSISVGLGRH 358  
 QY 331 PALLEKVLASDLPLPRKAKGKYTPKASSTVPEFTDPEYLLTITPTPTVTPQPSL 390  
 DB 359 PALLEKVLADLPLPRKAKGKYNCEAAACINCPGELREYLDLVKPKGHLMEPSL 418  
 QY 391 LNPSSISLSPPEPPLEPIESTIDPFSLAKQYPIPSUNLVEFASSSNWSKAA 450  
 DB 419 LNPSSISLSPLEPTEPEVETAPPELLAKQPSDSQSI NLVPTPASP-----DWG 471  
 QY 451 PSVYCPDLPNPKDVGKTIIVTGDLNLSLLNFKAAZLNLCGRKSPQFES-VASPSYVS 510  
 DB 472 PSMPHQVNDGGNTALAFNGG-----CS 496  
 QY 511 TPVENVVPVLSHLSIGSENSEHELLALSBPMCHVNNLPFVRGSLIRKPNFISLIGRI 570  
 DB 497 LPPSANMPP-----QNMKASNQLEAAPNAPFISQPVNRRANRELGLDGDGM 544  
 QY 571 VIPWTDLDLREKIGASSTIVYRGHWGSGVAVKILITQDRPHRPVNFELPEVAIMKSLP 630  
 DB 545 DIPWCDLNLKRIKIGASSETVHPAPHWGSDVAVKILMEQDRHAEFVNEFIPVAINKRIP 604  
 QY 631 HPRVLEWGAVKIRHLSIVITYSSGSLVELEHPSQVKEIDETPTTMAPFVAPQRRY 699  
 DB 605 HPRVLEWGAVQVFNLSIVLILSSGSLYELHNSGAELELEFELKELSMAYLVAKGMRY 664  
 QY 690 LHESLFVYHRELASHNLVIFKATVRYVTEGLESFLFAKTEFLSSKAACTLEMAFEVLF 749  
 DB 665 LHNKPELVHGLASPNLVAKYLVKVDGULSKKASIFLSSKSAAGIPEWMAFEVLR 724  
 QY 750 DEPSNEKSVYTSVTEMLATLQGWNLNPAQVAAVAVCPKGRLEIFPDVNFKLASI 809  
 DB 725 LEPSSKSLVSAVSLVLELALQLQFQWNLNPAQVAAVAVCPKGRLEIFENLQVAAV 784  
 QY 810 VAWALAEKRSFSSIMELGKSNPKQALPQGGETD 845  
 DB 785 EELWTEFQKRSFATIKGLLELILFEAVPFEED 820



DB 545 DTPWDLNKEKIGASSEVTVHIAEINHSSEVAVVILMEQDQIHAEVPEVEFLPEVAIMZPLP 604  
 QY 631 HPIVIMFGAVIKPPNLSIVTEVLSKGSYRLHKSGVKD-IDETIRINMAFDVAKGMNY 689  
 DB 605 HPIVIMFGAVIGFHEISVTEVLSKGSYRLHKSGVKDIDETIRINMAFDVAKGMNY 664  
 C7 605 HPIVIMFGAVIGFHEISVTEVLSKGSYRLHKSGVKDIDETIRINMAFDVAKGMNY 649  
 DB 665 LHKRNPVLRDLKSPNLLVKKRYTVKVDGEGISPKASTFLSSKSAAGTPEWMAPEVLR 724  
 QY 750 MPESNKSAYSESEVILWELALIGLQWNLNPAVVAAGVSEKGEPLIPPIVNDPLASLI 809  
 DB 725 DEFSNKSUVYSGVILWELALIGLQWNLNPAVVAAGVSEKGEPLIPPIVNDPLASLI 784  
 QY 810 VAWADEPKPKPSFSSTMETIKPMTKOAPDQSPD 845  
 DB 785 EGQWNEPKPKPSFATIMDLRLPKSAVDPENKSD 820  
 EAA50437  
 ID AAB50437 standard; Protein: 933 AA.  
 XX  
 AC AAB50437.  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE  
 XX Arabidopsis thaliana EDRI.  
 XX Arabidopsis thaliana, edr1, enhanced disease resistance; anti fungal,  
 KW antibacterial; gene therapy; transgenic plant; pathogen.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WC200071696-A1.  
 XX  
 PD 30-NOV-2000.  
 XX  
 PF 26-MAY-2000; 2000WO-0514718.  
 XX  
 PR 26-MAY-1999; 9905-0135895.  
 XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
 PA Innes RW, Frye CA;  
 XX  
 PI  
 PR  
 DR WPI; 2001-025156/03.  
 DE R1-PR; AA50434  
 XX  
 PT New gene EDRI of Arabidopsis thaliana, the disruption of which enhances  
 PT disease resistance in plants, is useful for producing transgenic plants  
 PT and mutants having increased resistance to plant pathogens.  
 XX  
 PS Claim 5; Fig 2, 91pp, English.  
 XX  
 CC The present sequence is that in a specification relating to the EDRI  
 CC gene located on Arabidopsis thaliana chromosome 1 between markers  
 CC ABE41 and MCG1. The disruption of the EDRI gene is associated with  
 CC enhanced resistance of a plant to plant pathogens or other  
 CC disease causing agents. A mutated transgene comprising the EDRI gene  
 CC mutated at residue 696 of the kinase encoding domain may be introduced  
 CC into the plant genome to reduce expression of EDRI. Alternatively, a  
 CC transgene that expresses part or all of an antisense strand of the EDRI  
 CC gene may be introduced. A transgene which expresses a sense strand of  
 CC the EDRI gene may be introduced to produce fertile Arabidopsis thaliana  
 CC plants. Transgenic plants exhibiting the desirable phenotypes of  
 CC lack of EDRI protein, EDRI mRNA, or enhanced resistance to plant  
 CC pathogens can be used for plant breeding, or directly in agricultural or  
 CC horticultural applications. Plants containing one transgene may also be  
 CC crossed with plants containing a complementary transgene in order to  
 CC produce plants with enhanced or combined phenotypes. EDRI nucleic acids  
 CC may be used as probes to detect the presence and/or expression of EDRI  
 CC genes and to identify related genes from other plant species.

XX Sequence 933 AA:  
 SQ  
 Query Match 28.28; Score 1250; DB 22; Length 933;  
 Best Local Similarity 34.7%; Pred. Rel. Acc. 100;  
 Matches 315; Conservative 128; Mismatches 277; Indels 189; Gaps 23;  
 QY BC SLSSEYVAITLSHAAAREINALEYITHTVFFVFAVCSAAVSTKFWAKGTFESVQLQD 149  
 DB 57 SSMASD--AHTAASNADYMS--EEYVQVLAALASASNS--SETEKHCRAA 139  
 QY 145 LVRLSSGTCADDNFMDPIDEAALRLSLSAFALSHREWNVNWSYLEKVKHGHVLI 205  
 DB 108 TLLSLGSHQ-----MDREK-----SEVVAQLSGLVYVYVVEEYVSY 155  
 QY 206 RMDYVVMVLTQNIQVCPIDSPSEIKTVMSFSSFFVVIQDSSKASEFQVNRVNI 205  
 DB 154 ----DVSLSTDSAKGEMPSLEULESHNCTD--FEAVVNVREHNSLHETLEANT 106  
 QY 256 ZSEVTT FEVACHAEALWTHLMSVSPNTPDVGVPELLEKLEKLVDAVLEL 125  
 DB 207 ALGCSFTSVSVLVQPLAEIVTEHMS--AEPSIVIAWTEKSEFAALNIVPELGV 205  
 QY 324 SVGGRHRAALLKVLASDLALCKAKGFRCTETLAAAGVAVAKRETLTGLDGL 169  
 DB 256 KGLSHPALERVLAEVLELFLVKLSQYTNELGAVNINLEHRETLVLEMLDGL 125  
 QY 384 LQDQ-----SLLNPSISISDPL 405  
 DB 325 LIPACTASA--NLVEPNSNINKEFLAQSEVKEKLSLSSSSQWARSSEKRETA 385  
 QY 404 R-----EPKLPSTIDF--ESLAKQVFLQSDINLVEFLASSNVVS--KIDAFSVQ 455  
 DB 386 EFTTSYPRVGLPN--DYSSPSVTSSTGCHNS SLATKLGKALFLKRLHRRVLP 445  
 QY 456 -----EPLNPEVT-----ETIVTDETESESLNPFYAAQ 488  
 DB 444 YQNSSEPEVNLPAQLPTLCKKGAQGYMLFES--RNVLEHLEPNSLVKGLAMWV 505  
 QY 489 -----NTQWRKSPQ-----PES 501  
 DB 504 NYSNFAPEKENSYLENLPRLHREKYSCTGATTCGHDALSSQWVSGRWVTPR 501  
 QY 502 VASPSVAST-----PEVNVV-----PESHSHSESESEH 552  
 DB 564 VAPSPSTSDENFRPSIVDMNNTNNTDGLPGLAAVVAAGVAGNLSHHRKYSGL 625  
 QY 634 LTAISHPM--PIVNNIPFVSSGLDEPNEL--SLGLEHVIPTGLDLEKLGASGLV 591  
 DB 624 ISTGLPEKDHSTSSLDSTSYPNPQVLLDAAWSECELPWNI VIAPKGLASGLV 585  
 QY 637 YRGTWESGVAVYLTGTHHFEVSPTELEVA--MESSEHRAVLEPM--AVETENISVI 651  
 DB 684 YIADWERTEVAVKFLDQDLSGAALATNSEVTRMERLHRVVTLCATVETPESVI 745  
 QY 652 EYLSPESEYELKESVETIDTTERIDMAITVAP--MAYDEEPEVHNSP--KESLAV 711  
 DB 803 NMNVKWEFLESEKENTFUSSTAGTTEWMAFEVLENEKAVISVNVIIWELAT 862  
 QY 772 GAEVWNLGALVVAAVYKQKPELLEPFAVNPPEASE--VA--WAKREKSGE--THET 851  
 DB 863 LELPWKRNQVGVGAGVGNEMFLPKETDPVVAWPIIPW--ETDNEK--KESLALEVR 922  
 QY 832 PMTKQAPP 839  
 DB 923 PLNRVLVP 930  
 RESULT 6









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 30.68;

Score 584.5; DB 21;  
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QY	599	GTVVRGHWGSDVAVKIIETQPHDPVNNEIPFVAVMKSLPHNIVLPMCAVTKPDNL 649

1P	127	500	HACTVTCGVAIKFIEHGVNNEMISPSQGVVMEKAVGKNAVVEKCAVTRSHLD 199
27	543	AVTELEFELLYELLDFGVESLDTTEFNHAFVASEIMTEDEEITFVNEDEKTHL 308	
DB	187	IVTFEMARGSYDFHKKCAIKLQILKVALVAKNSYLHGNLEHREIKIANLE 243	
QY	709	VKKTKVAVTQGLSKLKARTFLSSKSAATLMMATLVKLSGKGVTSNATVME 708	
DB	244	MEERHLVAVAFQVAVRQVTSQVNTAUSTEYVMMHEDVDEHVSRENAVVAVME 502	
27	719	LATVQPMENHFAVVAACITPQKELDIFEAIVNIEKATLVANALVDEHPSSEME 828	
DB	303	LLTGMLPYALFLPLQAAVGVCKGLPKTKKHPKAVKGLLEWQVQRELEPHE 392	
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KW	termination sequence.		
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QY 573 ---- PWDTDFPS----KZAGSPQZYVEEHCSEVAVPILTEQDFHEEV---- 616
DB 74 EGLVNYEWT IGLKLMGPAFAAGAFKNIYCTYNGELVAIKLERSUSNPEKAQALE 131
QY 617 HETFEIVAKSKS:PHH:VLPLGAVAKPTNLSIVTYLSPGSLVE:LFHFSVKRLLETFE 672
DB 132 QGQSQVSMALAFIKHENIVFICATKPMVMCTVTPYAKGSGVQFITEKQNPADVFLA 191
QY 677 INNAFIVAKMNTLHEPDPPEIVHEDLKSPNLIYKRYTVKVGDFGLSKLAPTFLSSKSA 736
DB 192 VMGALLIVAKMAVHVEH---FHHHFKSTHLLSAFSTKIADPEVAFIEVQT PHTTF 219
QY 737 AGTEWMAPEVLKDEPSNERSDYVSFGVILWELATIQQPMCNLPAQVAAVGGKGRKLD 796
DB 249 TGIYRWMAPEMIGHREYVLKVDYVSFGVILWELITGLIPQNMITAVQAAFAVAVNGVHPT 308
QY 797 ITRDVPKILASLIVACWADEPKWRPSPSSIMETLK 831
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RESULT 13
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AC AAG22171:
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 24998.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridization assay; gene expression; gene expression control; promoter,
KW termination sequence
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OS Arabidopsis thaliana.
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PN EP1013405-A2.
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PD 06 SEP-2000.
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PF 25 FEB-2000; 2000EP-0301439.
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PR 20-AUG-1999; 990S-0149723.  
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PR 23-AUG-1999; 990S-0149902.  
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PR 27-AUG-1999; 990S-0151065.  
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PR 30-JUN-1999; 990S-0141287.
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PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161992.
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PR 29-OCT-1999; 990S-0161994.
PR 29-OCT-1999; 990S-0162142.

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Query Match

Best Local Similarity 31.78; Score 510.5; DB 21; Length 407;

Matches 129; Conservative 72; Mismatches 141; Indels 59; Gaps 11;

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QY 468 IVYGDGRN - SOLINKRAASNTLOKRSSTAFKSVASSTSEPEVNVVL 120
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DE 9 VLAAGNHNNNNYAFQEFYQKLNCSNMISMQIRSVMS VIN 16

QY 521 SUTSHDSESEHLLSHDPZOHVRLPTVENSCTKRTNLSLGLHIVT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 56 -----SVSSVA TGHSTLPFVHFCTLVCSVSE TSVTLMSCALAGLDEP 107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 -----PWTDLRE-----KUGASRPIVYRGMHSGSVAVK 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 108 VFTGLGNYDWT IDLEKLMHGFAPAGAGAKYKSTYNGEDVAK 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 617 -NEFLFEVAKMSLEHPIVIFMGAVIFDPISTVTVFSEFPEVLEHFE 120
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DB 167 FMEQFQFQVSMILANKHPNIVRFIGACRKIMWVTVTEYAKGNSVK 220
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QY 674 TETINMAFTVAKGMNTHKEFPIVHCELSFNLNIPKSVAVN 111
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DB 227 KLVAKLALIVAKMAVYVGN--FTHGDKSNITLSAKSEIKIAUFVAV 284
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DB 284 TPETGIYRWMAPEMIQHRAYNKVDVYSFGIVIMELTIGLLPFQNM 448
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QY 794 RLDIPRNVTKLASLVACWAEHKEFSEFINETIK 841
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14 04 RETVING LEVISED MICHIGAN DEBROCKEVENVILLE 381

Search completed: October 22, 2002, 12:23:26  
Job time : 64 secs























Genome version 5.1.2  
Copyright (c) 1994 - 2002 Computer Ltd.

EM protein - protein search, using SW model

Run on: October 22, 2002, 10:43:45, Search time 25 Seconds  
(without alignments)  
1316.465 Million cell updates/sec

Title: US-09-904-389-2  
Sequence: 4435  
1 MEMOGPSPVSHLSLSTLPDP

EMPROGADPQSPDTLSVM R50

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40 \*

Fold. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2742.5	61.8	921	1	CTRL_ARATH
2	494	10.9	1584	1	KYSL_PICOL
3	467.5	10.5	755	1	KRAE_HUMAN
4	466.5	10.5	954	1	M3GA_HUMAN
5	463.5	10.5	410	1	FYFE_PICOL
6	463	10.4	323	1	KPAE_MCVIC
7	462.5	10.4	648	1	KRAE_FAT
8	462	10.4	806	1	RMIL_CHICK
9	462	10.4	927	1	RMIL_GALJA
10	460	10.4	328	1	KRAE_MOUSE
11	460	10.4	467	1	RMIL_AV111
12	460	10.4	450	1	RMIL_AVEVR
13	457.5	10.3	648	1	KRAE_HUMAN
14	457	10.3	647	1	KMIL_CHICK
15	453.5	10.2	638	1	KRAE_XENLA
16	453	10.2	1130	1	ARHL_HUMAN
17	451	10.2	380	1	FMIL_AVIWP
18	451	10.2	1123	1	ARHL_MOUSE
19	449	10.1	1182	1	ARHL_HUMAN
20	448	10.1	494	1	M3K9_HUMAN
21	447	10.1	781	1	KRAE_DROME
22	444.5	10.0	859	1	M3K6_HUMAN
23	444.5	10.0	888	1	M3K6_MOUSE
24	444	10.0	746	1	ABL_MLVAE
25	444	10.0	1520	1	ABL_DROME
26	442.5	10.0	882	1	M3K2_FAT
27	437.5	9.9	439	1	ABL_FSHVY
28	432	9.7	575	1	BMIL_HUMAN
29	428	9.7	613	1	KRAE_CAEEEL
30	424	9.6	604	1	KRAE_FAT
31	421	9.5	437	1	KRAA_MOUSE
32	421	9.5	606	1	KRAA_PIG
33	420	9.5	606	1	KRAA_HUMAN

34	414	9.3	536	1	FYN_XIDRF
35	409	9.2	942	1	IMEL_GALJA
36	406.5	9.2	505	1	FEZ_PICOL
37	405	9.1	536	1	FYN_XENLA
38	402.5	9.1	635	1	YBE_PICOL
39	399.5	9.0	536	1	FYN_HUMAN
40	399.5	9.0	590	1	RIKL_DROME
41	397	9.0	452	1	ILK_MOUSE
42	397	9.0	533	1	FYN_CHICK
43	396	8.9	452	1	ILK_HUMAN
44	396	8.9	579	1	M3K7_MOUSE
45	394.5	8.9	1196	1	ARHL_CAEEEL

ALIGNMENTS

RESULT 1  
CTRL\_ARATH STANDARD: PRI: 821 AA.  
AC 005600;  
DI 01-NOV-1995 (Rel. 32, Created)  
DI 01-NOV-1995 (Rel. 32, last sequence update)  
DI 16-DEC-2001 (Rel. 40, last annotation update)  
DE Serine/threonine-protein kinase CKII (P02711, 1-47).  
GN CTRL OR A15303730 OR F17615\_150.  
OS Arabidopsis thaliana (Mouse ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosales;  
OC Geraniales; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_F4810-4702;  
RN 111  
RP SEQUENCE FROM N.A.  
RC SUBAIN-IV, COLUMBIA; TISSUE Seedling;  
RX MEDLINE 93161417; PubMed 8431946;  
EA Kober J.J., Gothenberg M., Roman C., Erdmann R.A., Sweet J.K.  
ET CKII, a negative regulator of the ethylene response pathway in  
RL Cell 72:427-441(1993).

PP SEQUENCE FROM N.A.  
RC SUBAIN-IV, COLUMBIA;  
RX MEDLINE 21010717; PubMed 11107117;  
EA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asanuma T.,  
EA Miyajima N., Fujimoto S., Kimura T., Hara J., Iwano T., Kawano K.,  
EA Kohara M., Matsumoto M., Hattori A., Makaki A., Nakayama S.,  
EA Nakasaki N., Nario K., Okumura S., Shino S., Tanouchi O., Wada T.,  
EA Watanabe A., Yamada M., Yasuda M., Sato S., Ito H., Hoshida M.,  
EA Huang E., Spierer G., Ghof H., Shandnessy A., Preston R.,  
EA Haberman R., Murray J., Johnson B., Kelland L., Nelson J.,  
EA Sreter E., Pepin K., Pich K., Pich K., Pich K., Pich K., Pich K.,  
EA Belter E., Gordin B., Cordes M., Courtney L., Courtney L., Courtney L.,  
EA Du H., Edwards J., Fryman J., Harkness B., Lamm E., Lamm E.,  
EA Leonard S., Meyer R., Mulvaney E., Mulvaney E., Mulvaney E.,  
EA Wagner M., Weller C., Weller C., Weller C., Weller C., Weller C.,  
EA Barnell L., Shah R., Rodriguez M., Ron S., Ron S., Ron S., Ron S.,  
EA Firestein K., Fink K., Fink K., Fink K., Fink K., Fink K.,  
EA Martensen K., McVernie W.R., Wilson K.K., Murphy J., Rader J.,  
EA Volkert G., Wambert R., Wambert R., Wambert R., Wambert R.,  
EA Fontana K., Fontana K., Fontana K., Fontana K., Fontana K.,  
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EA Landham S.A., McCullagh H., Robben J., Glynn J., Glynn J.,  
EA Kamsperger W., Wedler H., Balke W., Wedler H., Wedler H.,  
EA van Straten M., Dirksen W., Meekins P., Meekins P., Meekins P.,  
EA Weitzsaecker T., Rothe G., Rose M., Hant J., Hant J., Hant J.,  
EA Feldpausch M., Lamberth S., Villarroel R., Villarroel R.,  
EA Peck C., Peck C., Peck C., Peck C., Peck C., Peck C.,  
EA Schueler C., Zaccaria P., Moses H., W. Ryan M., Ryan M.,  
EA Schueler C., Zaccaria P., Moses H., W. Ryan M., Ryan M.,  
ET thaliana.  
RI Nature 408:923-926(2000).  
OC 1. FUNCTION. ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE  
CC PATHWAY.  
CC 1. CATALYTIC ACTIVITY: ATP -> a protein ADP + a phosphate + H2O.













Oct 23 08:22:52 2002

Best Local Similarity 35.6%; Pred. No. 7,50-23; Indels 45; Gaps 13;  
Matches 126; Conservative 64; Mismatches 119;

QY 50 ASPYSQSTPPVENVVPLSHIUGSDSEHLLALSHFMDHVRNLDFVIGSQLPKPNE 562  
DB 288 ASPALSSSP-NNLSPP----- GWSQKPTVPFAPAPPSCTQKKNK 330  
QY 563 LSHAGLEAVIPW ---TDLDEKICAGSGTIVYKRGHGSQVAVKILTEQDFHPHVRNE 618  
DB 331 RRGQRDSYVWEIASEYMLSTRGSGTIVYKRGHGSQVAVKILTEQDFHPHVRNE 389  
QY 619 FUREVALMSLRHPNIVLEMCATKPNLSIVLYTSHGSLYRLDIKSGVKDIDETR--- 675  
DB 490 FNEVAVLAKTRIVNILLPMGYMK-DNLALVTQWCKGSSSLAKHLH- -VCETKFGM 442  
QY 676 -KINMAPIVAKENYILKRGDQIVIRDEKSTFLVQKYEYVQVCTSPKIKARTPLSS 733  
DB 44 FQALPFAKQVACQMOVYHAKN--LTHQKMSKSLFHLGELFVLCDSCLATVSPWSSQ 500  
QY 744 --KSAACTPHMAPEVLR--DEPSNKSRYSCVILWELATLQDPWNLNPA-QVVA 787  
DB 501 QVEGPTSVLMMAPVEVPMNDNPFSSQSDVYSGTIVLYELMTGELDYSHINRDQIFEM 560  
QY 789 VYKPEFVTHPPVW PRASLVA--QWALGKRTSSTSMETLYPMTKQAP 838  
DB 561 VGRYASHDSKATKATPEAFGRFVAVAGVGVPEFHFFGLSTLQHSLEP 614

RESULT 9  
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ID Q04982;  
DI 01-FEB-1994 (rel. 28, Created)  
DI 01-FEB-1994 (rel. 28, Last sequence update)  
DI 16-OCT-2001 (rel. 40, Last annotation update)  
DI RMIL serine/threonine protein kinase (P02771 37).  
GN C-MIL.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID: 9041;  
RN [1]  
RP SOURCE FROM N.A.  
RC Tissue: lymphocytes, and fibroblasts;  
RX MEDLINE 93312427; PubMed=832553;  
RA Calabrocci L., Barnier J.V., Eychene A., Felder M.-P., Calothy G.,  
Marx M.;  
RT "Genomic organization and nucleotide sequence of the coding region of  
the chicken c-mil (B-rat-1) proto-oncogene";  
RL Biochem. Biophys. Res. Commun. 193:1324-1331 (1993).  
CC FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN  
NEURAL CELLS.  
CC 1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
CC 2- SUBCELLULAR LOCATION: Nuclear.  
CC 3- ALTERNATIVE PRODUCTS: 2 ISORFORMS; A LONG FORM (SHOWN HERE) AND A  
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC 4- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.  
CC 5- PIM: PHOSPHORYLATED.  
CC 6- SIMILARITY: BELONGS TO THE SHR/THR FAMILY OF PROTEIN KINASES.  
CC 7- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHOSPHO-ESTER AND DAG  
BINDING DOMAIN.  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation at  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DB EMBL: X67052; CAA47436.1;

PIR: JN0612; JN0612.  
DR HSSP: P04849; 1PAR.  
DR InterPro: IPR002219; DAG\_PE-bind.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003116; RBD.  
DR InterPro: IPR004040; SIV\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR IcdRef: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00140; DAG\_PE-bind; 1.  
DR Pfam: PF00069; kkinase; 1.  
DR Pfam: PF02196; RBD; 1.  
DR Pfam: PF02196; RBD; 1.  
DR PRINTS: PR00048; DAGFEDOMAIN.  
DR SMART: SM00109; C1; 1.  
DR SMART: SM00221; STYK; 1.  
DR SMART: PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
DR PROSITE: PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00128; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS00128; PROTEIN\_KINASE\_ST; 1.  
DR PROTO-ONCOGENE: Transferrase; Serine/threonine protein kinase;  
KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;  
KW Phospho-ester binding; phosphorylation.  
KW P-MAIN 122 129 POLY-SER.  
FT DOMAIN 235 280 PHOSPHO-ESTER AND DAG BINDING  
FT DOMAIN 235 280 CYS-RICH.  
FT DOMAIN 497 757 PROTEIN KINASE.  
FT RT-BIND 503 511 ATP (BY SIMILARITY).  
FT BINDING 523 523 ATP (BY SIMILARITY).  
FT ACT\_SITE 616 616 BY SIMILARITY.  
FT VARSPIC 493 432 MISSING (IN SHORT ISOFORM)  
FT VARSPLIC 493 432  
SQ SEQUENCE 806 AA; 89365 MW; 8F4E4D5274FB75C C67643

Query Match 10.4%; Score 462; DR 1; Length 806;  
Best Local Similarity 39.3%; Pred. No. 1,10-22;  
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDLVIPWTDLREKIGAGSPGTVYKRGHGSQVAVKILTEQDFHPHVRNE 627  
DB 488 DWEIPIAGITVQIGSGSGTIVYKRGHGSQVAVKILTEQDFHPHVRNE 646  
QY 628 SDRHPIVIFMGAVIKPPNISIVTELSRGSYKRLDESKVLEDEKINMAPIVAKM 687  
DB 547 KTHVNLILFMGYSTR-PQALVTQWCKGSSSLYHLHLDEK-FEMIKLIDFARQACM 644  
QY 688 NYLHRDPPVIRDELKSPNLLVSKYKTVKVDGCSLSPEKARTFLSS--KSAATFENAP 745  
DB 605 DYLIHAKS--LIHRDLKSNITFLHEDLVKIGEEALAVKSEWSGSGRGLTASSTLKNAP 692  
QY 746 EVLRDEPSNE--KSDVYSGVILWELATLQDPWNLNPA-QVVAAY--GKPKRDLER 799  
DB 663 EVIRMDKNIYSGSDVYAVGIVLYELMTGELDYSHINRDQIFEM 722  
QY 800 EVIRMDKNIYSGSDVYAVGIVLYELMTGELDYSHINRDQIFEM 807  
DB 723 EVIRMDKNIYSGSDVYAVGIVLYELMTGELDYSHINRDQIFEM 762

RESULT 9  
RMIL\_COTLJA STANDARD: PRT: 807 AA.  
ID RMIL\_COTLJA  
DI 01-FEB-1994 (rel. 28, Created)  
DI 01-FEB-1994 (rel. 28, Last sequence update)  
DI 16-OCT-2001 (rel. 40, Last annotation update)  
DI RMIL serine/threonine-protein kinase (P02771 37).  
GN C-BW11  
OS Coturnix coturnix japonica (Japanese quail).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;  
OC Coturnix.  
OX NCBI\_TaxID: 93334;  
RN [1]  
RP SEQUENCE FROM N.A.



```

Query Match          10.4%; Score 460; DB 1; Length 328;
Best Local Similarity 39.3%; Pred. No. 40-23;
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDLVIPWIDDLREKLGAGSGFTVYRGWHSIVAVKLLIQDHFHPRVNEFLKEVALMK 627
DB 10 DWDETHDQGLTVAGTQSGSGFTVYRGWHSIVAVKLLIQDHFHPRVNEFLKEVALMK 68
QY 628 SLRHPRIVLPMGAVTRFNLSTVIEILSGSLTELLHESAVKTEETEEERMPATLVAKGM 687
DB 69 KTRHVNILLPMGYSTK-PQLAIVTQWCESSSLVHHLLHLETK-FEMIKLIIILAQIAQGM 126
QY 688 NYLHREDEP-VHKDLSPNLLVKKYIVKVCDEGLSGLFAFLPSS--KSAAGTFEMWAP 745
DB 127 DYLLHAKS (IHDRKSNFIHEDITVKGIDGLAIVKSNWSGSHOPEQISLIMWAP 184
QY 746 EVLEGLSPNE--KSAVYSESVILWELATLQDQWHLNFA QVVAAV--GPKRKLIDIPR 799
DB 185 EVIRMQKNNPYSQSDVATAGVGLVLEMTQLQVTSN--NNEQGLIFMWVPEGLSPQLSKVP 244
QY 800 DVNPK-LAS-LVACWADMTWKRPSPSSIMELIKMTKQAP 838
DB 245 SNTFKAMKPRMAECLTFKFFPDERPLEPQILASIELLARSLEP 284

RESULT 11
RMIL_AVEVR
ID RMIL_AVEVR11 STANDARD; PRT: 357 AA.
AC P10533; Q85612; Q85613; Q85614;
DI 01-JUL-1989 (Rel. 11, Created)
DI 01-JUL-1989 (Rel. 11, Last sequence update)
DI 01-MAR-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase transforming protein kmil
DE (62-2,7,1,37).
GN V-RMIL.
OS Avian retrovirus IC10.
OC Viruses; Retrovirdae; Retroviridae; Avian type C retroviruses
OX NCHL_TaxID 11874;
PI [1]
SEQUENCE FROM N.A.
MEDLINE 89160254; PubMed 2537952;
RA Eychene A., Marx M., Bezelac P., Calothy G.;
RT "Complete nucleotide sequence of IC10, a retrovirus containing the
RT kmil oncogene transduced in chicken neuroretina cells infected with
RT avian retrovirus RAV-1."
RL Nucleic Acids Res. 17:1250-1250(1989).
RN [2]
RX SEQUENCE FROM N.A.
MEDLINE 89091077; PubMed 2850163;
RA Marx M., Eychene A., Lauzier D., Bechade C., Grisanti P.,
RA Bezelac P., Pessac B., Calothy G.;
RT "A novel oncogene related to c-mil is transduced by infection with an avian
RT neuroretina cells induced to proliferate by infection with an avian
RT lymphomatous virus."
RL EMBO J. 7:3369-3373(1988).
OX -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
OX -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL
OX POLYPROTEIN.
OX -1- SIMILARITY: REFERENCES TO THE SER/THR FAMILY OF PROTEIN KINASES.
OX MIL/RAF SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X13744; CAA32008.1; ALT_SEQ
CC EMBL: X13438; CAA11790.1; ALT_SEQ
CC PIR: S01645; TVFVMI.
CC BSSP: P01462; TPCK.

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DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR004040; STY_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PolyPhen: PolyPhen/threonine-protein kinase; Transferrase; Phosphatase
KW ATP-binding. 67 327 DO-TEIN KINASE.
KW DOMAIN 73 81 ATP (BY SIMILARITY).
KW NP_BIND 73 81 ATP (BY SIMILARITY).
KW BINDING 93 93 ATP (BY SIMILARITY).
KW ACT_SITE 186 186 BY SIMILARITY.
KW SEQUENCE 367 AA; 41023 MW; E147AFDECG9308A CRC64;
Query Match          10.4%; Score 460; DB 1; Length 328;
Best Local Similarity 39.3%; Pred. No. 40-23;
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDLVIPWIDDLREKLGAGSGFTVYRGWHSIVAVKLLIQDHFHPRVNEFLKEVALMK 627
DB 58 DWDETHDQGLTVAGTQSGSGFTVYRGWHSIVAVKLLIQDHFHPRVNEFLKEVALMK 114
QY 628 SLRHPRIVLPMGAVTRFNLSTVIEILSGSLTELLHESAVKTEETEEERMPATLVAKGM 687
DB 117 KTRHVNILLPMGYSTK-PQLAIVTQWCESSSLVHHLLHLETK-FEMIKLIIILAQIAQGM 174
QY 688 NYLHREDEP-VHKDLSPNLLVKKYIVKVCDEGLSGLFAFLPSS--KSAAGTFEMWAP 745
DB 175 DYLLHAKS (IHDRKSNFIHEDITVKGIDGLAIVKSNWSGSHOPEQISLIMWAP 242
QY 746 EVLEGLSPNE--KSAVYSESVILWELATLQDQWHLNFA QVVAAV--GPKRKLIDIPR 799
DB 233 EVIRMQKNNPYSQSDVATAGVGLVLEMTQLQVTSN--NNEQGLIFMWVPEGLSPQLSKVP 292
QY 800 DVNPK-LAS-LVACWADMTWKRPSPSSIMELIKMTKQAP 838
DB 293 SNTFKAMKPRMAECLTFKFFPDERPLEPQILASIELLARSLEP 452

RESULT 12
RMIL_AVEVR
ID RMIL_AVEVR STANDARD; PRT: 450 AA.
AC P27966;
DI 01-AUG-1992 (Rel. 23, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 01-MAR-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein kinase transforming protein kmil
DE (62-2,7,1,37).
GN V-RMIL.
OS Avian rous-associated virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirinae.
OX NCHL_TaxID 11950;
PI [1]
SEQUENCE FROM N.A.
MEDLINE 91251215; PubMed 1645786;
RA Felder M.P., Eychene A., Barnier J.V., Calothy G.;
RA Marx M.;
RT "Common mechanism of retrovirus activation and transduction of c-mil
RT and c-Rml in chicken neuroretina cells infected with Rous-associated
RT virus type 1."
RL J. Virol. 65:3643-3640(1991).
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL ENV
CC POLYPROTEIN.
CC -1- SIMILARITY: REFERENCES TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC
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DR PRINTS: PR00008; DAGPEBMAIN.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM_1; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR TRANSFERASE: Serine/threonine protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol ester binding; Phosphorylation; 3D-structure
FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 343 609 PROTEIN KINASE.
FT NP_BIND 455 463 ATP (BY SIMILARITY).
FT BINDING 475 475 ATP (BY SIMILARITY).
FT ACT_SITE 468 468 HYDROXYLATION (BY PAK2/PAR3).
FT MOTIFS 436 438 FHSFHSKRTATICH (BY PAK2/PAR3).
SQ SEQUENCE 648 AA; 73051 MW; EPR21B534971HC3 CRC64;

Query Match 10.48; Score 457.5; DB 1; Length 648;
Best Local Similarity 35.38; Pred. No. 1.6e-22;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;

QY 503 ASPYAVQSTPPFVNVVFLSHSHIGSDSEHLALSHPRMDHYNNLPFVHGSQLIKPNE 562
DB 288 ASUALSSNP-----KRLSPFESQKRTIPVACQERAP-----VSGTP--EKNKI 330
QY 563 LSLGLELLIPW-----TDLDLREKICAGSGFYVRCGEHSGDAVKILITQDDHPERVNE 618
DB 331 RRGQDSSYYWFLDASEVWLSLRLGSGSRTVYKKKWHG-DVAVKILKVVQDPTPEFOQA 389
QY 619 FLREVALMKSLRIIPNVLFMGAVTKFNLSTVIEYSEGLYELLHKSQVNPDPTR--- 675
DB 390 FENAVAV:PTPIVNIILEMYMKR-DNIALVTQWCPSSSLYKHG-----VQETKPFOM 442
QY 676 KIRMAP:VAKSMYLLHPDPPVIVHPPVVKSPNIVVKKYTVKVDGRLSPKARTFLSS 733
DB 443 EQLDIARQAQMDYVHAKN---IHRDMFEEN:FLHEGLTVFVCDPLATVSEWWSQSQ 500
QY 734 --KSAAGCTEWMAPEVLP---DEPSNEKSDVYSPGVIIWELATLOOPWCNINPA-OVVAA 787
DB 501 QVPTQSGVLWMAPEVIRMQUNNIPSPQSVYSVGLVIFMTGELDYSHINRDQILFM 560
QY 788 VQKESGSLDPEAVN--PELASHIVA-CWAVHFWKPSSESMETLKMPKQAP 838
DB 561 VGRASASLSEYKRP-EEQFTLVAV:VVFVETETETIPFOTLSESTFLOHSLP 614

RESULT 14
KMIL_CHICK
ID KRAL_CHICK STANDARD: PRT: 647 AA.
AC P05625;
DE 01-NOV-1988 (Rel. 09, Created)
DE 01-NOV-1988 (Rel. 09, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE M16: protein serine/threonine protein kinase (sw 2.7.1.37)
GN C-MILK
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID:9031;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: Erythroblast;
PX MIM:TMF88217299; PubMed 4285296;
RA Kacoun M., Slippel A.E., Trachmann C., Bister K.;
RF "Primary structure of the chicken c-mil protein: identification of
RF domains shared with or absent from the retroviral v-mil protein.",
RF Oncogene 2:179-185(1988)
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: BELONGS TO THE SHP/RAF FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: BELONGS TO THE SHP/RAF SUBFAMILY.

-1- SIMILARITY: CONTAINS 1 ZINC PROPEPTEP PHORBOL-ESTER AND DAG
BINDING DOMAIN.
CC
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EMBL: X07017; CAA30069.1;
PIR: S00644; S03644.
HSP: P04049; IFAR.
InterPro: IPR002219; DAG_PE-bind.
InterPro: IPR00719; Euk_Pkinase.
InterPro: IPR004116; RBD.
InterPro: IPR004040; STY_Pkinase.
InterPro: IPR002290; Ser_Thr_Pkinase.
Pfam: PF00130; DAG_PE-bind; 1.
Pfam: PF00069; Pkinase; 1.
Pfam: PF02196; RBD; 1.
PRINTS: PR00008; DAGPEBMAIN.
SMART: SM00109; C1; 1.
SMART: SM00455; RBD; 1.
SMART: SM00221; STYKC; 1.
PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_DOM_1; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
TRANSFASER: Serine/threonine protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 343 609 PROTEIN KINASE.
FT NP_BIND 455 463 ATP (BY SIMILARITY).
FT BINDING 475 475 ATP (BY SIMILARITY).
FT ACT_SITE 468 468 BY SIMILARITY.
SQ SEQUENCE 647 AA; 73124 MW; RE1443667412HFO CRC64;

Query Match 10.48; Score 457; DB 1; Length 647;
Best Local Similarity 39.28; Pred. No. 1.7e-22;
Matches 114; Conservative 58; Mismatches 51; Indels 38; Gaps 11;

QY 566 GLLGVIVTP--TDLLEKIKGASGFIYVRCGEHSGDAVKILITQDDHPERVNE 621
DB 334 GQRGSSAVWLLASLVWLSRLGSGSRTVYKKKWHG-DVAVKILKVVQDPTPEFOQA 389
QY 622 VVALHPSGDEHRLIV:FWCAVTEPH:SLVTVYLCESVYVAV:VQVETETETIPFOTLSESTFLOHSLP 614
DB 393 EVAVLEKTRHVNILLEMYMKR-DNLAIVTQWCPSSSLYKHG-----VQETKPFOM 442
QY 677 INSAF:VAKSMYLLHPPDPPVIVHPPVVKSPNIVVKKYTVKVDGRLSPKARTFLSS 733
DB 446 IDIARQAQMDYVHAKN---IHRDMKSNNT:FLHEGLTVFVCDPLATVSEWWSQSQ 600
QY 735 SAAGCTEWMAPEVLPKQIFSR--KSAVSHGVIIWELATLOOPWCNINPA-OVVAAV 786
DB 504 QVPTQSLWMAPEVIRMQUNNIPSPQSVYSVGLVIFMTGELDYSHINRDQILFM 560
QY 791 KPEKESLDFEAVN--PELASHIVA-CWAVHFWKPSSESMETLKMPKQAP 838
DB 564 GLASEFLSRLGKRTETKRELVALGCTPEVETETETIPFOTLSESTFLOHSLP 614

RESULT 15
KRAF_XENIA
ID KRAF_XENIA STANDARD: PRT: 648 AA.
AC P04560; P99190;
DE 01-MAR-1989 (Rel. 10, Created)
DE 01-MAR-1989 (Rel. 10, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE KAF: proto-oncogene serine/threonine protein kinase (sw 2.7.1.37)

```











QY	374	LIEELGRKGGQAQTUPELLEKCPESISSESLRTRKRKIDESTLDRSLAKAYTHDSQSMLI	433
DB	476	VVBLIGEPNVHDPDISSINCEITQCQPSPQLMSHL-----	510
QY	134	VTPFAAGSNNVCCKKAAPAVYSSEPTTFFPACCTLVTTFTFPRSQLHPKAAQLENTAQG	493
DB	511	-----TDSPRCVHSTSPQTV-----FSKTSKTUSENIORSOSOOQ	547
QY	194	KSRQF-----RSICVASPSYVSQSTPFENVVPLSHISHIGSED-----S	531
DB	548	VHKFEFLPONAGTCVCAHIDIQUCCAKVSSMWLTESVLRALPID-IPNLSEEKIAPIQETCK	606
QY	532	EHLIALSHIP-----RMQHVNLLPFVHGSQLRKPNELSGLIEDIVI	572
DB	607	EEIVLLEDPTAMKKQPNLSVEPFIERADTEPKFGPLPYDATALSYCL--TIEPSLASDWLEV	664
QY	573	PWTFIDLDERKIRGASPGTWPPRFHWGSCTVAWAFTITQDPHPFPVAFPIPE-----	627
DB	665	SNNELHIKERVAGSGSVHRAFWHCSEVAVAKILLSIQDFHDVQPFEELEFVCKQAVAIMK	724
QY	628	SLKHNPVILEMGAVTKPPNLSIVTYEYLSNGSLRYRLHKSSVKD-IDETRIMWAEDEV---	683
DB	725	RVDHPNWVLMFGAVTERPHSIITIFLYLPESSTFPIHPFASSELLDQPEFLKMAEDVVCA	784
QY	684	---ARGMNYLHRKDUPPIVERHOLSKFNILLVDKKYTKVGVDFGLSRLKARTFLSSKSAAGT	739
DB	785	IPIYAKGLNYLR-LNPVVVMDLKSFNLLVDXNMWIKVGVDFGLSRLKANTFIPSKSVAGT	844
QY	740	PEMKAREVLDREPSNEKSDVYSGVILWEALATQQPMCNLNPAQVVAVGFKCRKLDIR	799
DB	845	PEMKAREVLCRPENKSDVYSGVILWEALATQQPMCNLNPAQVVAVGFKCRKLDIR	804
QY	900	TVPKPIASTIVA-WAQRWKPSSESSIMELEIKMTFOAPTQ	840
DB	905	NISPVLVSLMEAWDEPSLRPAFNSIVTLKLIK-SPVQ	944
RESULT 6			
ID	Q9FTR4	PRELIMIRAKY	FRT 533 AA
AC	Q9FTR4		
DC	01-MAR-2001	(JEMR rel 16, created)	
DT	01-MAR-2001	(JEMRrel 16, last sequence update)	
DT	01-JUN-2001	(JEMRrel 19, last annotation update)	
DE	BRL		
DE	ECR1		
CN	ERY1		
OC	Arabidopsis thaliana (Mouse ear cross).		
OC	Eukaryota; Viridiplantae; Eutracheophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid1; Brassicales; Brassicaceae; Arabidops.		
NCBI_TaxId	3702		
SEQUENCE	N.A.		
MDLINE	21325153; RefSeq 11114160		
PROJ	FLY C.A., Tang D., Innes R.W.		
RT	"Neutrophil regulation of cytokine responses in mouse by a conserved MAPKK kinase";		
INTPROT	IPR000719; Puk_pkinase,		
INTPROT	IPR002249; Ser_thr_kinase,		
INTPROT	IPR004040; STY_pkinase,		
PFAM	PF00669; pkinase; 1,		
PRINTS	PR0109; TyrcNAZ,		
SMART	SM00221; STYK; 1,		
SMART	SM00220; S-TK; 1,		
SMART	SM00219; TyrKC; 1,		
POSTITE	PS00107; PROTEIN_KINASE_ATP; 1,		
POSTITE	PS0011; PROTEIN_KINASE_DOM; 1,		
ATP-binding	Transferrase		
SEQUENCE	943 AA; 10388 MW; 650EF2FF0B41205D7 CRC64;		









[illegible]



Q7 151 YLF LMEKLVGKTIYVTELEIRGGLAKKA ..... 122  
 Db 419 FAETPPNATEAKRSSTAFKNNNSDFRPPENVVPPSAPSQPLVKKNSACNDISN 478  
 Q7 436 AQTETAPG ..... EFPFSGVAVSYVQSTPEVE ..... 515  
 Db 479 NKQYNVAIGSVPPFNATINASSSMIAISIAKHYN-----PNVPTLNPMYAAPAPNYDNPI 534  
 Q7 516 ..... NVPLSHISHIGSD ..... 530  
 Db 535 IGTSAMAKASTGICIDRSQVPPCLYYDKMGTSSMNTASSSGIGKVAEKDLQNDLEKGP 594  
 Q7 541 ..... SEHLALSHRDMHVNKL-----PFVHGSOLIR-----KPN 561  
 Db 595 YSRFAGLAKSKNAQCTPPEPRDEIKENCGSYDHEMLHPDPKPSPIIDPMIDPRONIECVSPS 654  
 Q7 562 ELSLGIDPLV-----IPWTDLDERIGAGSEFYVYRGEMHGSDVAVKILTEQDFHP 613  
 Db 655 QWGSKKVPLVDEVSECLLWEDLVIDEKIGIGSYGEVYHADWNGTEVAVKRFLOQFPYG 714  
 Q7 614 ERVNEFLREVAIMKSLRHPNIVLFWCAVIKPPNLSIVITYLSRGSLYRLHLKSGVKDIDK 673  
 Db 715 DALLEFRGCVETMPPLRHPNIVLFWCAVITPPHLSIVSEYLERGSLYRIIHRPNCQ-IDE 773  
 Q7 674 TPRINMAFPVAKSMNLYHPPROPPIVHPDLKSPNLLVDKKYTVKVQDPFGLSRKARTFLSS 733  
 Db 774 KRRIKMALDVARGMNCILHISVPTVHRDLKSPNLLVDQNTVKKVQDPFGLSRKHSFLSS 833  
 Q7 734 KSACTPWWMAPEVLRLDPSNEKSDVSPGVITWELATLQQWCNINPACVVAAGFKGK 793  
 Db 844 KSTACTPWWMAPEVLRLDPSNEKSDVSPGVITWELATLQRKPMHGMNQVGVGAVGQDR 893  
 Q7 794 RLDIPRONPKIASLIVACWADPEWPKRPSSESSIMETLKDMTKOAPPOOSPT 844  
 Db 894 RLDIPKEVDPIVASILRLQWQKDPNLRPSFTQLTSYKLTQRLVLPDSHOET 944  
 REF0114  
 Q9LM42 ..... 583 AA  
 AC Q9LM42 ..... 583 AA  
 DI C1-OCT-2000 (Trembl) 15, Last sequence update)  
 DI C1-OCT-2000 (Trembl) 15, Last sequence update)  
 DE C1-DEC-2001 (Trembl) 19, Last annotation update)  
 DE C1-DEC-2001 (Trembl) 19, Last annotation update)  
 OS Arabidopsis thaliana (Mammalian cross).  
 OC Euphydia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Malvales; Euphorbiales; Euphorbiaceae; Euphorbia  
 OC Euphorbia; Brassicales; Brassicaceae; Arabidopsids.  
 OX RefSeq: EF021792.  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Shinn P., Brooks S., Buchler E., Chao Q., Johnson Hopson C., Khan S.,  
 RA Kim C., Altieri D., Bel S., Chao Q., Chao J., Chao E., Chang L.,  
 RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,  
 RA Long C., Liu J., Liu K., Liu S., Liu S., Makharsky N., Nguyen M.,  
 RA Palm C., Pham P., Sakane H., Schwartz J., Southwick A., Thayer A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.  
 RA Genomic sequence for Arabidopsis thaliana BAC T19422 from chromosome  
 RT 1.  
 FC 5,600 bp  
 CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AC069551; AA787373.1.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR002290; Ser\_Thr\_Pkinase.  
 DR InterPro: IPR004040; STY\_Pkinase.  
 DR InterPro: IPR001245; Ty\_Pkinase.  
 DR Pfam: PF00069; Pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_DOM; 1.  
 SW All-Seed-Set: 30.38, Score 1057.5, DR 10; Length 988;  
 SQ SEQUENCE 988 AA; 107398 MW; RD4075595596FHI CR64;  
 Query Match 23.88; Score 1057.5; DR 10; Length 988;  
 best Local Similarity 33.38; Pred. No. 2.66 70;  
 Matches 315; Conservative 129; Mismatches 288; Indels 309; Gaps 44;  
 QY 36 GGVNKKRTPDVPDPMSGDHRI-----NLQAVRIGNIVSWTGLQGH-SNCSVYDSSSS 60  
 Db 22 GGVNKKRTPDVPDPMSGDHRI-----NLQAVRIGNIVSWTGLQGH-SNCSVYDSSSS 60  
 QY 91 DYVAPILSNPAANEINALEYILDDGFVKKAVSG-----GSSSKSWAATFESFQGLPL 146  
 Db 91 DYVAPILSNPAANEINALEYILDDGFVKKAVSG-----GSSSKSWAATFESFQGLPL 146  
 QY 82 DFTTHREAGVCSH ..... SDMGAGGAGGCRGRIHEVEFYQIQ 114  
 Db 82 DFTTHREAGVCSH ..... SDMGAGGAGGCRGRIHEVEFYQIQ 114  
 QY 117 VGRGCTVETZAGTINPDPIHTEA ALKGLGAG ..... AGAGTHREAGG 174  
 Db 117 VGRGCTVETZAGTINPDPIHTEA ALKGLGAG ..... AGAGTHREAGG 174  
 QY 121 ALHETGA RRPD FAAGTHAEQGLDGRIRAPDITPAIMATKMYKMYNVL 168  
 Db 121 ALHETGA RRPD FAAGTHAEQGLDGRIRAPDITPAIMATKMYKMYNVL 168  
 QY 193 SYLFFVPGVGYLTHFMDPYVWSLTATNIGPD-----PDSFESKLVSSSLAVVL 268  
 Db 193 SYLFFVPGVGYLTHFMDPYVWSLTATNIGPD-----PDSFESKLVSSSLAVVL 268  
 QY 169 GYHKKIVGCV ..... DLDGVNLSSEKREHFAVAGGLVAVLAVHGVVSS 219  
 Db 169 GYHKKIVGCV ..... DLDGVNLSSEKREHFAVAGGLVAVLAVHGVVSS 219  
 QY 251 STASLKELQNEVHNI ..... SSSGVITKIVAVHIAKLVNHREAVVETHTLVSAK 303  
 Db 251 STASLKELQNEVHNI ..... SSSGVITKIVAVHIAKLVNHREAVVETHTLVSAK 303  
 QY 219 KDSNLRLRQWALDIAAKKFASSSGVSTAVGLANVAVNMSHVD 477  
 Db 219 KDSNLRLRQWALDIAAKKFASSSGVSTAVGLANVAVNMSHVD 477  
 QY 304 RGSNDPFCGLSASVPLSLEVGLCPHALLFVLAISLHLPFPAKPKYTHIGAS 461  
 Db 304 RGSNDPFCGLSASVPLSLEVGLCPHALLFVLAISLHLPFPAKPKYTHIGAS 461  
 QY 279 SLSYSLKATLPSWPLQSLTGLAPHALLFVLAISLHLPFPAKPKYTHIGAS 461  
 Db 279 SLSYSLKATLPSWPLQSLTGLAPHALLFVLAISLHLPFPAKPKYTHIGAS 461  
 QY 362 -----SCLVRFGLD-----REYLDLGRPGTLCQDHS 412  
 Db 362 -----SCLVRFGLD-----REYLDLGRPGTLCQDHS 412  
 QY 338 SIKTFDSSGRLFSLINPNVNFYIVDMGHPNILLFAPAGLQMLHFNYSVSSDP 439  
 Db 338 SIKTFDSSGRLFSLINPNVNFYIVDMGHPNILLFAPAGLQMLHFNYSVSSDP 439  
 QY 403 -----LFFRL----- 408  
 Db 403 -----LFFRL----- 408  
 QY 397 GSHVASSGCVISCTHIFESKVAHREFTLREELFALMELNTRHEAV 434  
 Db 397 GSHVASSGCVISCTHIFESKVAHREFTLREELFALMELNTRHEAV 434  
 QY 465 ..... KLPSTHQAALIA ..... NLTLDG ..... GQGVAVGGA 490  
 Db 465 ..... KLPSTHQAALIA ..... NLTLDG ..... GQGVAVGGA 490  
 QY 457 TVGLSEFTHTFTFAESTSWTEVAVGLAHREAVLVSRLHAEFLMGLAFHMD 490  
 Db 457 TVGLSEFTHTFTFAESTSWTEVAVGLAHREAVLVSRLHAEFLMGLAFHMD 490  
 QY 429 SSGVAVSGKAAASVYQFPAKRVISCKLVVLIKESNLGKAEAAALNI QKSKS 490  
 Db 429 SSGVAVSGKAAASVYQFPAKRVISCKLVVLIKESNLGKAEAAALNI QKSKS 490  
 QY 517 LSSVVAIPNLFSAV ..... SLSMAGLGRKVAALNKKLFTPLNAGKNS 563  
 Db 517 LSSVVAIPNLFSAV ..... SLSMAGLGRKVAALNKKLFTPLNAGKNS 563  
 QY 497 QTESVATYVVAETIV ERVVLQIHE ..... LGLLHLELAEHEDR 543  
 Db 497 QTESVATYVVAETIV ERVVLQIHE ..... LGLLHLELAEHEDR 543  
 QY 567 RGLIVKTLTLLRFGSKATLHLRHSAGAGHCHGCHGCHGCHGCHGCHGCHGCHG 622  
 Db 567 RGLIVKTLTLLRFGSKATLHLRHSAGAGHCHGCHGCHGCHGCHGCHGCHGCHG 622  
 QY 546 NNLP-----FVHGSOLI ..... 633  
 Db 546 NNLP-----FVHGSOLI ..... 633  
 QY 623 ERHVEVAVAAAVASVAAAKVAFVLTLLTAAAVAAVAAVAAVAAVAAVAAVAAVAAV 682  
 Db 623 ERHVEVAVAAAVASVAAAKVAFVLTLLTAAAVAAVAAVAAVAAVAAVAAVAAVAAV 682  
 QY 558 -----RKPNLSLGLF-----GLVTPWGLDRIKFAISEFI 590  
 Db 558 -----RKPNLSLGLF-----GLVTPWGLDRIKFAISEFI 590  
 QY 683 GDAAGGLHGVDSGERSISKSNSSKSDAAHDAVATLHREHVAERKIGUNSI 742  
 Db 683 GDAAGGLHGVDSGERSISKSNSSKSDAAHDAVATLHREHVAERKIGUNSI 742  
 QY 591 VYSEMEKSTV AVETLEASCHPFTVHTLENAKKELEHNAVLEAVTEHREH 649  
 Db 591 VYSEMEKSTV AVETLEASCHPFTVHTLENAKKELEHNAVLEAVTEHREH 649  
 QY 649 ..... SATLVMAVKKELQGLDGLAALL ..... KATKIKMSI 705  
 Db 649 ..... SATLVMAVKKELQGLDGLAALL ..... KATKIKMSI 705  
 QY 650 VTEVLSGSLYKILRKSQVREIDELRGNMAIVAKGKQDLSKSGFYANRGRGPNILV 709  
 Db 650 VTEVLSGSLYKILRKSQVREIDELRGNMAIVAKGKQDLSKSGFYANRGRGPNILV 709  
 QY 784 VTELPFSTVETLREPH RPTDFPPEPMALZAFWYTHGSHVAREKSERILV 842  
 Db 784 VTELPFSTVETLREPH RPTDFPPEPMALZAFWYTHGSHVAREKSERILV 842  
 QY 710 GRKIVKVLTELSKLAELTSSKZAGTLEWALVLEKLEPSSVAVSGVLTWEL 769  
 Db 710 GRKIVKVLTELSKLAELTSSKZAGTLEWALVLEKLEPSSVAVSGVLTWEL 769  
 QY 843 DKNVAVAVDGLSKMKVSYLSSKSLAGLAERMAFVLRNPAVENTVSYGVLTWEL 902  
 Db 843 DKNVAVAVDGLSKMKVSYLSSKSLAGLAERMAFVLRNPAVENTVSYGVLTWEL 902  
 QY 770 ATACAGWNTNPAVVAAVTPKGFETPTFVPIVLAELVAVWALWELRSTGIMEI 829  
 Db 770 ATACAGWNTNPAVVAAVTPKGFETPTFVPIVLAELVAVWALWELRSTGIMEI 829



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 22, 2002, 12:22:46 ; Search time 25 Seconds  
(without alignments)  
830.470 Million cell updates/sw

Title: US-09-904-389-2

Perfect score: 4435

Sequence: 1 MEMPKRSDYSLLSQIPDEF .....KMPFKAPQSQSTPTDYSVM 650

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:

1: US-07-928-464-2 (A-OMP Ref)  
2: US-08-955-841-6 (A-OMP Ref)  
3: US-08-955-841-5 (A-OMP Ref)  
4: US-08-955-841-4 (A-OMP Ref)  
5: US-08-955-841-3 (A-OMP Ref)  
6: US-08-955-841-2 (A-OMP Ref)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2742.5	61.8	821	1	US-07-928-464-2
2	2742.5	61.8	821	1	US-08-033-311B-2
3	2742.5	61.8	821	1	US-08-955-841-2
4	2742.5	61.8	821	5	PCP-0593-07347-2
5	1191.5	26.9	264	3	US-09-035-706-5
6	1191.5	26.9	264	3	US-08-955-841-5
7	1191.5	26.9	264	3	US-08-390-425-5
8	504.5	11.4	455	3	US-09-221-235-5
9	504.5	11.4	455	3	US-09-221-928-5
10	504.5	11.4	455	4	US-09-221-527-5
11	504.5	11.4	455	4	US-09-221-236-5
12	504.5	11.4	455	4	US-09-221-416-5
13	504.5	11.4	455	4	US-09-221-245-5
14	504.5	11.4	455	4	US-09-163-115-5
15	504.5	11.4	455	4	US-09-221-528-5
16	504.5	11.4	455	4	US-09-593-553-5
17	504.5	11.4	455	4	US-09-221-237-5
18	468	10.6	648	1	US-08-185-282-4
19	465	10.5	648	1	US-08-185-282-1
20	464	10.4	648	1	US-08-185-282-2
21	460	10.4	648	1	US-08-185-282-3
22	457.5	10.3	648	1	US-08-276-151-2
23	457.5	10.3	648	1	US-08-185-283-1
24	457.5	10.3	648	2	US-08-886-751A-6
25	457.5	10.3	648	3	US-09-209-668-13
26	457.5	10.3	648	4	US-08-971-207-1
27	456	10.3	271	3	US-09-035-706-6

28 456 10.3 271 3 US-08-955-841-6  
29 456 10.3 271 4 US-09-490-425-6  
30 455 10.3 346 1 US-08-276-151-5  
31 446 10.1 315 1 US-08-571-758-12  
32 446 10.1 315 1 US-08-909-984A-12  
33 446 10.1 315 1 US-08-909-984-12  
34 444.5 10.0 668 1 US-08-205-018-2  
35 444.5 10.0 859 1 US-08-395-580-2  
36 444.5 10.0 859 5 PCP-0595-02792-2  
37 441 9.9 267 2 US-07-857-224B-42  
38 438 9.9 275 2 US-08-701-191A-30  
39 438 9.9 648 1 US-08-185-282-5  
40 436 9.8 261 2 US-07-857-224B-59  
41 436 9.8 261 2 US-07-857-224B-60  
42 432 9.7 675 4 US-08-426-509A-4  
43 432 9.7 675 5 PCP-0595-05008-4  
44 415.5 9.4 267 2 US-07-857-224B-45  
45 414 9.3 635 1 US-08-571-758-10

#### ALIGNMENTS

##### RESULT 1

US-07-928-464-2

; Sequence 2, Application US/07928464

; Patent No. 5367065

; GENERAL INFORMATION:

; APPLICANT: Ecker, Joseph R.

; APPLICANT: Kieber, Joseph J.

; TITLE or INVENTION: Constitutive Intra Response Gene and

; TITLE or INVENTION: Mutations

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESS: Woodcock, Washburn, Kurt Z. Mackiewicz and

; ADDRESS: No. 540/065115

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.05

; CURRENT APPLICATION DATA: 05/97/225.464

; APPLICATION NUMBER: 05/97/225.464

; FILING DATE: 19920810

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Miller, Suzanne E.

; REGISTRATION NUMBER: 22,279

; TELEPHONE: 215-568-3100

; TELECOMMUNICATION INFORMATION:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 821 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-07-928-464-2

Query Match 61.8% Score 2742.5; DB 1; Length 821;

Best Local Similarity 62.48; Pred. No. 2,440,247;

Matches 546; Conservative 141; Indels 87; Gaps 14;

QY 1 MEMPKRSDYSLLSQIPDEFV3---TCASFSYFVSVA---ADWIKRTER VII-49

DB 1 MEMPKRSDYSLLSQIPDEFV3---TCASFSYFVSVA---ADWIKRTER VII-49

QY 50 WD GSGHRLNTQATRIC-NLY-SKGLQKSSSSYDLSLSSSYVALTSSNPAN 104





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DB 545 DTHWDLNKKAGSGGTVHRAEWHGSDVAVKILMEQDPHAEKRVNEFTREVAIMKRLR 604
QY 641 HFNVLVEMGAVTKRFFNLSTVITLSKSGATKLLHAKGVKD-10ETKKINMAFDVAKGMNY 689
DB 605 HFNVLVEMGAVTKRFFNLSTVITLSKSGATKLLHAKGVKD-10ETKKINMAFDVAKGMNY 664
QY 696 HHROROPAVHROIKSPNITVKKYTVGVVDFGLSELKAPTEFLSKSAAGTTEWMAPEVLR 749
DB 665 HHROROPAVHROIKSPNITVKKYTVGVVDFGLSELKAPTEFLSKSAAGTTEWMAPEVLR 724
QY 750 DEFSNEKSDVYSGVILWELATLQPCWNLNPAQVAAVGGFKGKRLDIPRIVNEPKLASLI 809
DB 725 DEFSNEKSDVYSGVILWELATLQPCWNLNPAQVAAVGGFKGKRLDIPRIVNEPKLASLI 784
QY 810 VACWADEPKWRKPSFSIMETLKMTEQADPQQSRID 845
DB 785 EFWTNEPKWRKPSFSIMETLKMTEQADPQQSRID 820

```

## RESULT 3

US 08 261-442-2

Sequence 2, Application US/0926-1442

Patent No. 5602422

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene

TITLE OF INVENTION: and Mutations

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Farkas, Mackiewicz and

ADDRESS: No. 5602422rls

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0926-1442

FILING DATE: June 17, 1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,311

FILING DATE: January 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardsell

REGISTRATION NUMBER: 34,293

REFERENCE/INVENT NUMBER: UPN-1864

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-261-442-2

Query Match 61.8%; Score 2742.5; DB 1; Length 821.

Best local Similarity 62.4%; Pred. No. 2,4e-237;

Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;

QY 1 MEMORSDYSLSLSDIPDEEVG---TGASTSEYDSVAA-----CGNVKIGTDP-VPD 49

DB 1 MEMPGRRNNTLLSOFSDQVSVSVIGAPPHIYDSLSENKSNHNSGNTGKAKAERGFD 60

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QY 50 WDA---GNDGDFRTAVRIS HCY PGLNLEHRAKSNVTVVAVLADNATATILSNKAA 100
DB 61 WDA---GNDGDFRTAVRIS HCY PGLNLEHRAKSNVTVVAVLADNATATILSNKAA 100
QY 104 FINALTYILIDDFRV-----MKAVASAG--SSSKSWAQHIESKLEQGVIRL 150
DB 120 ELESVGPIDGDFRGGGGGGLPQMAADSAKNSSSSSSWAQHIESKLEQGVIRL 150
QY 151 SSKAWACAPNEMDIPDANALKGLLEALASHREWNKMGAVLKKVKNLILILIMOP 210
DB 180 SSKAWACAPNEMDIPDANALKGLLEALASHREWNKMGAVLKKVKNLILILIMOP 210
QY 211 YWSELCTRIQETPPTSTESTETVSS LFFTVVULREKAGLKKRKRVRITSSVY 270
DB 240 YWSELCTRIQETPPTSTESTETVSS LFFTVVULREKAGLKKRKRVRITSSVY 270
QY 271 TPIVAVHAKLVGNHIGSSVSGELDIASANKENLLEKELGSAVILKSLGSAVILK 330
DB 300 TPIVAVHAKLVGNHIGSSVSGELDIASANKENLLEKELGSAVILKSLGSAVILK 330
QY 331 KALLKVLADSLHAGCRFARGKCYCTRPAASGLVRLGRLALDILKPKRDAQDST 390
DB 359 KALLKVLADSLHAGCRFARGKCYCTRPAASGLVRLGRLALDILKPKRDAQDST 390
QY 391 LNDSSLSLSSDIPPRDIPPESTIDPPQAKAVTIDVGLVTEASERVVTELDA 450
DB 419 LNDSSLSLSSDIPPRDIPPESTIDPPQAKAVTIDVGLVTEASERVVTELDA 450
QY 451 EFWTNEPKWRKPSFSIMETLKMTEQADPQQSRID 845
DB 472 EFWTNEPKWRKPSFSIMETLKMTEQADPQQSRID 820
QY 511 TPFVNVVVLSHLSHIGSENSEHLLALSHDPMRHHVNNIDYVHRKQLERENLSHLE 570
DB 497 LPPSANMPP-----QNMKRASNIKAATINNAHPSQVFNKAKRKLHSDIM 630
QY 571 VTPWTVDPKTCASSTVYSGEMDQVAVKLEKCTPHRWNNLEKAVAKESKR 630
DB 545 DIPWEDLINEKELCAGSCTVHPACWHGSDVAVKILMEQDPHAEKRVNEFTRE 604
QY 641 HFNVLVEMGAVTKRFFNLSTVITLSKSGATKLLHAKGVKD-10ETKKINMAFDV 689
DB 605 HFNVLVEMGAVTKRFFNLSTVITLSKSGATKLLHAKGVKD-10ETKKINMAFDV 664
QY 696 HHROROPAVHROIKSPNITVKKYTVGVVDFGLSELKAPTEFLSKSAAGTTEWMA 749
DB 665 HHROROPAVHROIKSPNITVKKYTVGVVDFGLSELKAPTEFLSKSAAGTTEWMA 724
QY 750 DEFSNEKSDVYSGVILWELATLQPCWNLNPAQVAAVGGFKGKRLDIPRIVNEPK 809
DB 725 DEFSNEKSDVYSGVILWELATLQPCWNLNPAQVAAVGGFKGKRLDIPRIVNEPK 784
QY 810 VACWADEPKWRKPSFSIMETLKMTEQADPQQSRID 845
DB 785 EFWTNEPKWRKPSFSIMETLKMTEQADPQQSRID 820

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## RESULT 4

PCT-US93-07347-2

Sequence 2, Application PCT/US93-07347

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene and

TITLE OF INVENTION: Mutations

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Farkas, Mackiewicz and

ADDRESSEE: Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.





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? ? EARLIER APPLICATION NUMBER: 09/16,411
? ? EARLIER FILING DATE:
? ? NUGGET TYPE: INVENTION
? ? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 5
? LENGTH: 455
? TYPE: PRT
? ORGANISM: Homo sapiens
? CDS: 1-421 / 235-4

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Query Match 11.48; Score 504.5; DB 3; Length 455;  
Best Local Similarity 40.98; Pred. No. 8.4e-47;  
Matches 112; Conservative 41; Mismatches 106; Indels 15

[illegible]

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RE:001  7
US 09-221 928 5
  1  SEQNUM 5  APPLICATION 0250221928
  2  PATENT NO 6121030
  3  GENUS 1  SPECIES 1
  4  APPLICANT  ACTION  Susan
  5  TITLE OF INVENTION  A NEW TYPE OF BATTERY
  6  FILE REFERENCE  MM 050
  7  PRIORITY  A1  A1  5  NUMBER  500  00000000  A1
  8  CURRENT FILING DATE  1998-12-28
  9  EARLIER APPLICATION NUMBER  097433300
  10  EARLIER FILING DATE:
  11  NUMBER OF SEQ ID NOS: 15
  12  SOFTWARE: Patent In Vol. 2.0
  13  SEQ ID NO 5
  14  LENGTH  455
  15  TYPE  FRT
  16  ORGANISM  Homo Sapiens
  17  US 09-221 928 5

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[illegible][illegible][illegible]

## RESUME

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RESULT 11
US-09-221-246-5
? Sequence 5, Application US-09-221-246
? Patent No. 6146841
? GENERAL INFORMATION
? APPLICANT: Action, Susan
? TITLE OF INVENTION: BEVEL GLASS
? FILE REFERENCE: MNI-050
? CURRENT APPLICATION NUMBER: US-09-221-246
? CURRENT FILING DATE: 1998-12-29
? EARLIER APPLICATION NUMBER: 09/165,115
? EARLIER FILING DATE: 1998-09-29
? NUMBER OF SEQ. ID NOS.: 15
? SOFTWARE: Pattern In Var., 2.0
? SEQ. ID NO. 5
? LENGTH: 455
? TYPE: Pkt
? REACTION: Hom. Saponins
US-09-221-246-5
Query Match

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Best Local Similarity 40.9%; Score 504.5; DB 4; Length 455;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVLPWTDLDLREKIGAGSEFTVYVGEWFGSP--VAVKTIIFQOQTHPEVRETFLE 621
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 3 SLGASFVQIKFDLQFFENCQSGSFGSVYFAKWIISQKQEVAVKRLKLE-----K 52

QY 622 EVAIMKSLRHNPILVFMGAVTKPPNISIVFYLSRGLSLRLHLKSGVKDKIDETRRINMAP 681
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNY 112

QY 682 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 740
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 113 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 170

QY 741 EWMAPEVLDRDPSNEKSDYVSFGVILWELATLOQPWCNINPAQVAAVGFGRKRLDIPRD 800
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 171 PWMAPEVIQSLPVSEFTDYSYGVVLWEMLTREVDFKGLQVAVLVEKNERLTIPSS 230

QY 801 VNPKLASLVACWADEPKRPSESSIMETIKPMT 834
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DB 231 CPRSFARLLHQCWEADAKKRPSPKQIISLESMS 264

RESULT 12
US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09221416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5

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Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Score 504.5; DB 4; Length 455;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVLPWTDLDLREKIGAGSEFTVYVGEWFGSP--VAVKTIIFQOQTHPEVRETFLE 621
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 3 SLGASFVQIKFDLQFFENCQSGSFGSVYFAKWIISQKQEVAVKRLKLE-----K 52

QY 622 EVAIMKSLRHNPILVFMGAVTKPPNISIVFYLSRGLSLRLHLKSGVKDKIDETRRINMAP 681
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNY 112

QY 682 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 740
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
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QY 741 EWMAPEVLDRDPSNEKSDYVSFGVILWELATLOQPWCNINPAQVAAVGFGRKRLDIPRD 800
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DB 171 PWMAPEVIQSLPVSEFTDYSYGVVLWEMLTREVDFKGLQVAVLVEKNERLTIPSS 230

QY 801 VNPKLASLVACWADEPKRPSESSIMETIKPMT 834
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DB 231 CPRSFARLLHQCWEADAKKRPSPKQIISLESMS 264

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RESULT 13
US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6160458

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; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09221245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: US/092163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-245-5

Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Score 504.5; DB 4; Length 455;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVLPWTDLDLREKIGAGSEFTVYVGEWFGSP--VAVKTIIFQOQTHPEVRETFLE 621
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DB 3 SLGASFVQIKFDLQFFENCQSGSFGSVYFAKWIISQKQEVAVKRLKLE-----K 52

QY 622 EVAIMKSLRHNPILVFMGAVTKPPNISIVFYLSRGLSLRLHLKSGVKDKIDETRRINMAP 681
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DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNY 112

QY 682 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 740
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DB 113 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 170

QY 741 EWMAPEVLDRDPSNEKSDYVSFGVILWELATLOQPWCNINPAQVAAVGFGRKRLDIPRD 800
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 171 PWMAPEVIQSLPVSEFTDYSYGVVLWEMLTREVDFKGLQVAVLVEKNERLTIPSS 230

QY 801 VNPKLASLVACWADEPKRPSESSIMETIKPMT 834
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DB 231 CPRSFARLLHQCWEADAKKRPSPKQIISLESMS 264

RESULT 14
US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-115-5

Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Score 504.5; DB 4; Length 455;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVLPWTDLDLREKIGAGSEFTVYVGEWFGSP--VAVKTIIFQOQTHPEVRETFLE 621
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DB 3 SLGASFVQIKFDLQFFENCQSGSFGSVYFAKWIISQKQEVAVKRLKLE-----K 52

QY 622 EVAIMKSLRHNPILVFMGAVTKPPNISIVFYLSRGLSLRLHLKSGVKDKIDETRRINMAP 681
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DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNYGVILEPPNY 112

QY 682 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 740
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DB 113 DVAKGMNYLHRDPP-PIVHRDLKSPNLIIVDKKYTVKVCDCGLSRFKARTFLSSKSAAGTP 170

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